STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number 119788

TO: Olga Chernyshev **Location: rem 4e84 & 4c70** **Art Unit: 1646** **Wednesday, April 21, 2004** **Case Serial Number: 09/919473**	**From: Toby Port** **Location: Biotech-Chem Library** **Remsen 1A59** **Phone: 571-272-2523** **toby.port@uspto.gov**

Search Notes

Dear Examiner Chernyshev,

Here are the results of your search.
Please feel free to contact me if you have any questions.

Toby Port

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 20, 2004, 18:51:47 ; Search time 18.24 Seconds
(without alignments)
657.330 Million cell updates/sec

Title: US-09-919-473-11
Perfect score: 179
Sequence: 1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	88	49.2	151	13	Q9I8E5	Q9i8e5 fugu rubrip
2	60	33.5	42	6	O77577	O77577 ovis aries
3	60	33.5	209	11	Q9DC90	Q9dc90 mus musculu
4	57	31.8	165	13	Q7ZZM1	Q7zzm1 spea hammon
5	57	31.8	187	11	Q8CIT0	Q8cit0 mus musculu
6	57	31.8	191	6	Q8HZV1	Q8hzv1 sus scrofa
7	56	31.3	162	13	Q8UUH6	Q8uuh6 cyprinus ca
8	56	31.3	1795	4	Q9P2B8	Q9p2b8 homo sapien
9	53.5	29.9	270	3	Q9P781	Q9p781 schizosacch
10	53	29.6	69	6	O77778	O77778 ovis aries
11	53	29.6	279	2	Q8KZR5	Q8kzr5 pseudomonas
12	53	29.6	279	16	Q88RA2	Q88ra2 pseudomonas
13	53	29.6	417	16	Q98LJ7	Q98lj7 rhizobium l
14	52.5	29.3	492	16	Q88KI0	Q88ki0 pseudomonas
15	52.5	29.3	802	5	Q8SZ78	Q8sz78 drosophila
16	52	29.1	161	13	Q7ZZL9	Q7zzl9 ameiurus ne
17	52	29.1	166	13	Q800D2	Q800d2 salvelinus
18	52	29.1	167	13	Q9I9D0	Q9i9d0 oreochromis
19	52	29.1	167	13	Q7SXA4	Q7sxa4 oncorhynchu
20	52	29.1	248	2	Q7X390	Q7x390 escherichia
21	52	29.1	393	10	O49567	O49567 arabidopsis
22	52	29.1	399	5	Q8SWJ8	Q8swj8 encephalito
23	52	29.1	494	16	Q7VSW0	Q7vsw0 bordetella
24	52	29.1	500	16	Q7WF51	Q7wf51 bordetella
25	52	29.1	500	16	Q7W3S3	Q7w3s3 bordetella
26	52	29.1	514	5	Q9VXL5	Q9vxl5 drosophila
27	52	29.1	1064	5	Q965L0	Q965l0 caenorhabdi
28	52	29.1	1275	5	Q9Y1H5	Q9y1h5 dictyosteli
29	51.5	28.8	464	2	Q93JT8	Q93jt8 pseudomonas
30	51	28.5	220	16	Q88ZY1	Q88zy1 lactobacill
31	51	28.5	412	16	Q9A254	Q9a254 caulobacter
32	51	28.5	817	10	Q7XSF1	Q7xsf1 oryza sativ
33	50.5	28.2	1093	10	Q84W30	Q84w30 arabidopsis
34	50.5	28.2	1325	10	O64533	O64533 arabidopsis
35	50	27.9	159	16	Q92D25	Q92d25 listeria in
36	50	27.9	343	16	Q7USE1	Q7use1 rhodopirell
37	50	27.9	416	13	Q9DDE2	Q9dde2 brachydanio
38	50	27.9	419	16	Q8UGT4	Q8ugt4 agrobacteri
39	50	27.9	485	16	Q88T41	Q88t41 lactobacill
40	50	27.9	523	10	Q7XEM4	Q7xem4 oryza sativ
41	50	27.9	1065	16	Q81BF4	Q81bf4 bacillus ce
42	50	27.9	1082	5	Q95U36	Q95u36 drosophila
43	50	27.9	1325	5	Q9VP80	Q9vp80 drosophila
44	50	27.9	1887	12	Q9IMS9	Q9ims9 cherry mott
45	49.5	27.7	105	16	Q9CLE7	Q9cle7 pasteurella

ALIGNMENTS

RESULT 1
Q9I8E5
ID Q9I8E5 PRELIMINARY; PRT; 151 AA.
AC Q9I8E5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Urocortin precursor.
GN UCN.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetradontoidea; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20485066; PubMed=11032317;
RA Brunner B., Gruetzner F., Yaspo M.L., Ropers H.H., Haaf T.,
RA Kalscheuer V.M.;
RT "Molecular cloning and characterization of the Fugu rubripes
RT MEST/COPG2 imprinting cluster and chromosomal localization in Fugu and
RT Tetraodon nigroviridis.";
RL Chromosome Res. 8:465-476(2000).
DR EMBL; AJ251323; CAB96535.1; -.
KW Signal.
FT SIGNAL 1 20 POTENTIAL.
SQ SEQUENCE 151 AA; 16686 MW; EEB1D52C41A67124 CRC64;

Query Match 49.2%; Score 88; DB 13; Length 151;
Best Local Similarity 47.2%; Pred. No. 4.5e-05;
Matches 17; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

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Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              ||||||  :: :| : |: |  |  :|| ||::|||:
Db        112 LSLDVPTNIMNVLFDVAKAKNLRAKAAENARLLAHI 147
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RESULT 2

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O77577
ID   O77577      PRELIMINARY;      PRT;    42 AA.
AC   O77577;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   UROCORTIN precursor (Fragment).
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Cepoi D., Sutton S., Vale W.W.;
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 14-42 FROM N.A.
RA   Baigent S.M., Lowry P.J.;
RT   "The cloning of ovine urocortin.";
RL   Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF051807; AAC27288.1; -.
DR   EMBL; AF084258; AAC33478.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR000187; corticoliberin.
DR   InterPro; IPR003620; Urocortin_CRF.
DR   Pfam; PF00473; CRF; 1.
DR   PRINTS; PR01612; CRFFAMILY.
DR   SMART; SM00039; CRF; 1.
DR   PROSITE; PS00511; CRF; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   42 AA;  4893 MW;  31D6139D4937C9E2 CRC64;

  Query Match             33.5%;  Score 60;  DB 6;  Length 42;
  Best Local Similarity   44.4%;  Pred. No. 0.17;
  Matches   16;  Conservative    5;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              ||:|:   ||| ||| || :: | :|  |   |  |
Db          5 LSIDLTFHLLRTLLELARTQSQRERAEQNRIIFDSV 40


RESULT 3
Q9DC90
ID   Q9DC90      PRELIMINARY;      PRT;   209 AA.
AC   Q9DC90;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   Proprotein convertase subtilisin/kexin type 4.
GN   PCSK4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Brain;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK003053; BAB22535.1; -.
DR   MGD; MGI:97514; Pcsk4.
SQ   SEQUENCE   209 AA;  22636 MW;  3ACFC611907DD17D CRC64;

  Query Match             33.5%;  Score 60;  DB 11;  Length 209;
  Best Local Similarity   50.0%;  Pred. No. 1.1;
  Matches   12;  Conservative    5;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          8 PIGLLRILLEQARYKAARNQAATN 31
              |:|| :  | |||| :|:| | |:
Db         98 PLGLRKAHLPQARYPSAQNHACTD 121


RESULT 4
Q7ZZM1
ID   Q7ZZM1      PRELIMINARY;      PRT;   165 AA.
AC   Q7ZZM1;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Corticotropin-releasing hormone precursor.
GN   CRH.
OS   Spea hammondii (western spadefoot toad).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pelobatoidea; Pelobatidae;
OC   Spea.
OX   NCBI_TaxID=228670;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Boorse G.C., Denver R.J.;
RT   "Endocrine mechanisms underlying plasticity in metamorphic timing in
RT   spadefoot toads.";
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY262255; AAP20883.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR000187; corticoliberin.
DR   InterPro; IPR003620; Urocortin_CRF.
DR   Pfam; PF00473; CRF; 1.
DR   PRINTS; PR01612; CRFFAMILY.
DR   ProDom; PD005970; Urocortin_CRF; 1.
DR   SMART; SM00039; CRF; 1.
DR   PROSITE; PS00511; CRF; 1.
KW   Signal.
FT   SIGNAL        1     24       Potential.
FT   CHAIN       123    163       corticotropin-releasing hormone.
SQ   SEQUENCE   165 AA;  18443 MW;  D7A3B7F5BC810EF4 CRC64;

  Query Match             31.8%;  Score 57;  DB 13;  Length 165;
  Best Local Similarity   39.4%;  Pred. No. 2.3;
  Matches   13;  Conservative    8;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQIL 35
              :|||:   ||| :|| || :    || :| :::
Db        128 ISLDLTFHLLREVLEMARAEQIAQQAHSNRKLM 160


RESULT 5
Q8CIT0
ID   Q8CIT0      PRELIMINARY;      PRT;   187 AA.
AC   Q8CIT0;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Preprocorticotropin-releasing hormone.
```

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OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RA   Seasholtz A.F., Bourbonais F.J., Harnden C.E., Camper S.A.;
RT   "Nucleotide Sequence and Expression of the Mouse Corticotropin-
RT   Releasing Hormone Gene.";
RL   Mol. Cell. Neurosci. 2:266-273(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RA   Seasholtz A.F., Bourbonais F.J., Harnden C.E., Camper S.A.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY128673; AAN07905.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR000187; corticoliberin.
DR   InterPro; IPR003620; Urocortin_CRF.
DR   Pfam; PF00473; CRF; 1.
DR   PRINTS; PR01612; CRFFAMILY.
DR   ProDom; PD005970; Urocortin_CRF; 1.
DR   SMART; SM00039; CRF; 1.
DR   PROSITE; PS00511; CRF; 1.
FT   CHAIN       145    187       CORTICOTROPIN-RELEASING HORMONE.
SQ   SEQUENCE   187 AA;  20778 MW;  5E51665291FAA998 CRC64;

  Query Match             31.8%;  Score 57;  DB 11;  Length 187;
  Best Local Similarity   39.4%;  Pred. No. 2.7;
  Matches   13;  Conservative    8;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQIL 35
              :|||:   ||| :|| || :    || :| :::
Db        150 ISLDLTFHLLREVLEMARAEQLAQQAHSNRKLM 182


RESULT 6
Q8HZV1
ID   Q8HZV1      PRELIMINARY;      PRT;   191 AA.
AC   Q8HZV1;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Corticotropin releasing hormone.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22027062; PubMed=12030933;
RA   Wimmers K., Murani E., Ponsuksili S., Schellander K.;
RT   "Sequence variation and linkage mapping of the porcine corticotropin
RT   releasing hormone (CRH) gene.";
RL   Anim. Genet. 33:233-234(2002).
DR   EMBL; AF440229; AAN40888.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR000187; corticoliberin.
DR   InterPro; IPR003620; Urocortin_CRF.
DR   Pfam; PF00473; CRF; 1.
DR   PRINTS; PR01612; CRFFAMILY.
DR   ProDom; PD005970; Urocortin_CRF; 1.
DR   SMART; SM00039; CRF; 1.
DR   PROSITE; PS00511; CRF; 1.
SQ   SEQUENCE   191 AA;  20969 MW;  507950FA0EAC9011 CRC64;

  Query Match             31.8%;  Score 57;  DB 6;  Length 191;
  Best Local Similarity   39.4%;  Pred. No. 2.8;
  Matches   13;  Conservative    8;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQIL 35
              :|||:   ||| :|| || :    || :| :::
Db        154 ISLDLTFHLLREVLEMARAEQLAQQAHSNRKLM 186


RESULT 7
Q8UUH6
ID   Q8UUH6      PRELIMINARY;      PRT;   162 AA.
AC   Q8UUH6;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Putative corticotropin releasing hormone precursor.
GN   CRH.
OS   Cyprinus carpio (Common carp).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Cyprinus.
OX   NCBI_TaxID=7962;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Macrophage;
RA   Huising M.O., van den Burg E.H., Verburg-van Kemenade L.B.M., Flik G.;
RT   "Expression of corticotropin releasing hormone (CRH) in the common
RT   carp (Cyprinus carpio L.).";
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ317955; CAC84859.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR000187; corticoliberin.
DR   InterPro; IPR003620; Urocortin_CRF.
DR   Pfam; PF00473; CRF; 1.
DR   PRINTS; PR01612; CRFFAMILY.
DR   SMART; SM00039; CRF; 1.
DR   PROSITE; PS00511; CRF; 1.
KW   Signal.
FT   SIGNAL        1    119       POTENTIAL.
FT   CHAIN       120    160       PUTATIVE CORTICOTROPIN RELEASING HORMONE.
SQ   SEQUENCE   162 AA;  18300 MW;  511DDBA0D1E2A5C9 CRC64;

  Query Match             31.3%;  Score 56;  DB 13;  Length 162;
  Best Local Similarity   39.4%;  Pred. No. 3.2;
  Matches   13;  Conservative    8;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQIL 35
              :|||:   ||| :|| || :    || :| :::
Db        125 ISLDLTFHLLREVLEMARAEQMAQQAHSNRKMM 157


RESULT 8
Q9P2B8
ID   Q9P2B8      PRELIMINARY;      PRT;  1795 AA.
AC   Q9P2B8;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein KIAA1429 (Fragment).
GN   KIAA1429.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=20181126; PubMed=10718198;
RA   Nagase T., Kikuno R., Ishikawa K., Hirosawa M., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes.XVI.
RT   The complete sequences of 150 new cDNA clones from brain which code
RT   for large proteins in vitro.";
RL   DNA Res. 7:65-73(2000).
DR   EMBL; AB037850; BAA92667.1; -.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
```

```
DR   InterPro; IPR000504; RNA_rec_mot.
DR   PROSITE; PS00030; RRM_RNP_1; 1.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   1795 AA;  200853 MW;  B26CDB49A6961063 CRC64;

  Query Match             31.3%;  Score 56;  DB 4;  Length 1795;
  Best Local Similarity   34.4%;  Pred. No. 52;
  Matches   11;  Conservative    6;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          6 DVPIGLLRILLEQARYKAARNQAATNAQILAH 37
              : |:|:||||||:   |   :|    :  |
Db       1684 EAPVGVLRILLEEITMKVVEARAILTEALFHH 1715


RESULT 9
Q9P781
ID   Q9P781      PRELIMINARY;      PRT;   270 AA.
AC   Q9P781;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   SPBC1711.09C.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972h-;
RA   Aert R., Volckaert G., Wood V., Rajandream M.A., Barrell B.G.;
RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL353012; CAB88239.1; -.
DR   GeneDB_SPombe; SPBC1711.09c; -.
KW   Hypothetical protein.
SQ   SEQUENCE   270 AA;  30067 MW;  0316EA38FEC30D37 CRC64;

  Query Match             29.9%;  Score 53.5;  DB 3;  Length 270;
  Best Local Similarity   34.9%;  Pred. No. 14;
  Matches   15;  Conservative   11;  Mismatches   10;  Indels    7;  Gaps    3;

Qy          1 VILSLDVPIGLLRILLEQARYKAARN---QAATN--AQILAHV 38
              ::||: | :| |  |:   |||| :|   : :||  : :| |:
Db        195 IVLSIVVTLGTLAFLI--VRYKAIKNSTLEDSTNSTSDVLNHL 235


RESULT 10
O77778
ID   O77778      PRELIMINARY;      PRT;    69 AA.
AC   O77778;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Urocortin (Fragment).
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Richardson M.P.;
RL   Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF085334; AAC35555.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR000187; corticoliberin.
DR   InterPro; IPR003620; Urocortin_CRF.
DR   Pfam; PF00473; CRF; 1.
DR   PRINTS; PR01612; CRFFAMILY.
DR   SMART; SM00039; CRF; 1.
DR   PROSITE; PS00511; CRF; 1.
FT   NON_TER       1      1
FT   NON_TER      69     69
SQ   SEQUENCE    69 AA;  8132 MW;  E437469148BC219A CRC64;

  Query Match             29.6%;  Score 53;  DB 6;  Length 69;
  Best Local Similarity   44.8%;  Pred. No. 3.4;
  Matches   13;  Conservative    5;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATN 31
              ||:|:   ||| ||| || ::   :|  |
Db         37 LSIDLTFHLLRTLLELARTQSQXERAEQN 65


RESULT 11
Q8KZR5
ID   Q8KZR5      PRELIMINARY;      PRT;   279 AA.
AC   Q8KZR5;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   ABC-type transporter membrane permease component.
GN   TAUC.
OS   Pseudomonas putida.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=303;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DS1;
RA   Endoh T., Kasuga K., Horinouchi M., Yoshida T., Habe H., Nojiri H.,
RA   Omori T.;
RT   "Characterization and identification of genes essential for dimethyl
RT   sulfide-utilization in Pseudomonas putida strain DS1.";
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM.
CC       PROBABLY RESPONSIBLE FOR THE TRANSLOCATION OF THE SUBSTRATE ACROSS
CC       THE MEMBRANE (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE BINDING-PROTEIN-DEPENDENT TRANSPORT
CC       SYSTEM PERMEASE FAMILY.
DR   EMBL; AB086390; BAC00966.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR000515; BPD_transp.
DR   Pfam; PF00528; BPD_transp; 1.
DR   PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; 1.
KW   Transmembrane; Transport.
SQ   SEQUENCE   279 AA;  29760 MW;  42FB5664C8133719 CRC64;

  Query Match             29.6%;  Score 53;  DB 2;  Length 279;
  Best Local Similarity   28.6%;  Pred. No. 17;
  Matches   12;  Conservative   12;  Mismatches   14;  Indels    4;  Gaps    1;

Qy          1 VILSLDVPIGLLRI----LLEQARYKAARNQAATNAQILAHV 38
              : |::  || :        :: |: :||::  || ||:: ||
Db        153 IYLAIFAPIAIATATGVRTVDPAKLRAAQSLGATKAQLIRHV 194


RESULT 12
Q88RA2
ID   Q88RA2      PRELIMINARY;      PRT;   279 AA.
AC   Q88RA2;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Taurine ABC transporter, permease protein.
GN   TAUC OR PP0231.
OS   Pseudomonas putida (strain KT2440).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=160488;
```

```
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22423060; PubMed=12534463;
RA   Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA   Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA   Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
RA   Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
RA   Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,
RA   Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
RA   Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
RA   Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA   Fraser C.M.;
RT   "Complete genome sequence and comparative analysis of the
RT   metabolically versatile Pseudomonas putida KT2440.";
RL   Environ. Microbiol. 4:799-808(2002).
DR   EMBL; AE016774; AAN65863.1; -.
DR   TIGR; PP0231; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR000515; BPD_transp.
DR   Pfam; PF00528; BPD_transp; 1.
DR   PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; 1.
KW   Complete proteome.
SQ   SEQUENCE   279 AA;  29858 MW;  A792078299F83F9C CRC64;

  Query Match             29.6%;  Score 53;  DB 16;  Length 279;
  Best Local Similarity   28.6%;  Pred. No. 17;
  Matches   12;  Conservative   12;  Mismatches   14;  Indels    4;  Gaps    1;

Qy          1 VILSLDVPIGLLRI----LLEQARYKAARNQAATNAQILAHV 38
              : |::  || :        :: |: :||::  || ||:: ||
Db        153 IYLAIFAPIAIATATGVRTVDPAKLRAAQSLGATKAQLIRHV 194


RESULT 13
Q98LJ7
ID   Q98LJ7      PRELIMINARY;      PRT;   417 AA.
AC   Q98LJ7;
DT   01-OCT-2001 (TrEMBLrel. 18, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Probable secretion protein.
GN   MLL0995.
OS   Rhizobium loti (Mesorhizobium loti).
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Phyllobacteriaceae; Mesorhizobium.
OX   NCBI_TaxID=381;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MAFF303099;
RX   MEDLINE=21082930; PubMed=11214968;
RA   Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA   Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA   Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA   Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA   Takeuchi C., Yamada M., Tabata S.;
RT   "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT   Mesorhizobium loti.";
RL   DNA Res. 7:331-338(2000).
DR   EMBL; AP002996; BAB48466.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0015428; F:type I protein secretor activity; IEA.
DR   GO; GO:0009306; P:protein secretion; IEA.
DR   InterPro; IPR006143; HlyD.
DR   InterPro; IPR003997; RtxD.
DR   Pfam; PF00529; HlyD; 1.
DR   PRINTS; PR01490; RTXTOXIND.
KW   Complete proteome.
SQ   SEQUENCE   417 AA;  43968 MW;  D4C33503BBA5B5ED CRC64;

  Query Match             29.6%;  Score 53;  DB 16;  Length 417;
  Best Local Similarity   46.4%;  Pred. No. 27;
  Matches   13;  Conservative    4;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          2 ILSLDVPIGLLRILLEQARYKAARNQAA 29
              : :||  | | | |:||||    |  ||:
Db        146 VRNLDAQIVLQRALIEQARATVAATQAS 173


RESULT 14
Q88KI0
ID   Q88KI0      PRELIMINARY;      PRT;   492 AA.
AC   Q88KI0;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Methyl-accepting chemotaxis transducer.
GN   PP2310.
OS   Pseudomonas putida (strain KT2440).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=160488;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22423060; PubMed=12534463;
RA   Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA   Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA   Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
RA   Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
RA   Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,
RA   Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
RA   Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
RA   Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA   Fraser C.M.;
RT   "Complete genome sequence and comparative analysis of the
RT   metabolically versatile Pseudomonas putida KT2440.";
RL   Environ. Microbiol. 4:799-808(2002).
DR   EMBL; AE016782; AAN67923.1; -.
DR   TIGR; PP2310; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0006935; P:chemotaxis; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR004089; Chmtaxis_transd.
DR   InterPro; IPR003660; HAMP.
DR   Pfam; PF00672; HAMP; 1.
DR   Pfam; PF00015; MCPsignal; 1.
DR   PROSITE; PS50111; CHEMOTAXIS_TRANSDUC_2; 1.
DR   PROSITE; PS50885; HAMP; 1.
KW   Complete proteome.
SQ   SEQUENCE   492 AA;  52127 MW;  D3594D62560AB198 CRC64;

  Query Match             29.3%;  Score 52.5;  DB 16;  Length 492;
  Best Local Similarity   55.6%;  Pred. No. 39;
  Matches   15;  Conservative    4;  Mismatches    7;  Indels    1;  Gaps    1;

Qy         11 LLRILLEQ-ARYKAARNQAATNAQILA 36
              |  : ||| || :||: |||  ||:||
Db         30 LYAVHLEQRARAEAAQAQAAAQAQLLA 56


RESULT 15
Q8SZ78
ID   Q8SZ78      PRELIMINARY;      PRT;   802 AA.
AC   Q8SZ78; Q9VA13;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   RE14222p (CG11318-PA).
GN   CG11318.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
RA Tupy J.L., Bergman C.M., Berman B.P., Carlson J.W., Celniker S.E.,
RA Clamp M.E., Drysdale R.A., Emmert D., Frise E., de Grey A.D.N.J.,
RA Harris N.L., Kronmiller B., Marshall B., Millburn G.H., Richter J.,
RA Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F.,
RA Whitfield E.J., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J.,
RA Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY071063; AAL48685.1; -.
DR EMBL; AE003776; AAF57115.2; -.
DR FlyBase; FBgn0039818; CG11318.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR000203; PKD_cys_rich.
DR Pfam; PF00002; 7tm_2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS50221; GPS; 1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
SQ SEQUENCE 802 AA; 90457 MW; D63E82D4F5DB521D CRC64;

Query Match 29.3%; Score 52.5; DB 5; Length 802;
Best Local Similarity 41.7%; Pred. No. 69;
Matches 15; Conservative 9; Mismatches 7; Indels 5; Gaps 2;

Qy 3 LSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
Db 511 LSL---LGILGIFLTAALFKSWRSQAST--KVLLHL 541

Search completed: April 20, 2004, 18:56:44
Job time : 20.24 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 20, 2004, 18:51:32 ; Search time 5.06667 Seconds
(without alignments)
390.526 Million cell updates/sec

Title: US-09-919-473-11
Perfect score: 179
Sequence: 1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	179	100.0	112	1	UCN2_MOUSE	Q99ml8 mus musculu
2	162	90.5	109	1	UCN2_RAT	Q91ww1 rattus norv
3	139	77.7	112	1	UCN2_HUMAN	Q96rp3 homo sapien
4	78	43.6	161	1	UCN3_HUMAN	Q969e3 homo sapien
5	75	41.9	164	1	UCN3_MOUSE	Q924a4 mus musculu
6	61	34.1	41	1	UR1_CATCO	P01145 catostomus
7	60	33.5	122	1	UCN1_MOUSE	P81615 mus musculu
8	60	33.5	122	1	UCN1_RAT	P55090 rattus norv
9	60	33.5	124	1	UCN1_HUMAN	P55089 homo sapien
10	60	33.5	145	1	UR1_CARAU	Q9ptq4 carassius a
11	60	33.5	145	1	UR1_CYPCA	P01146 cyprinus ca
12	60	33.5	165	1	UR1_ONCMY	O93448 oncorhynchu
13	57	31.8	162	1	CRF_XENLA	P49188 xenopus lae
14	57	31.8	187	1	CRF_RAT	P01143 rattus norv
15	57	31.8	191	1	CRF_PIG	P06296 sus scrofa
16	57	31.8	196	1	CRF_HUMAN	P06850 homo sapien
17	56	31.3	162	1	CRF1_CATCO	P13241 catostomus
18	56	31.3	162	1	CRF_CARAU	Q9ptsl carassius a
19	54	30.2	60	1	UR1_PLAFE	P21624 platichthys
20	54	30.2	162	1	CRF2_CATCO	P25308 catostomus
21	53	29.6	40	1	SAUV_PHYSA	P01144 phyllomedus
22	50	27.9	190	1	CRF_SHEEP	P01142 ovis aries
23	50	27.9	875	1	CND3_SCHPO	Q10429 schizosacch
24	49.5	27.7	633	1	MLH_TETTH	P40631 tetrahymena
25	49.5	27.7	2181	1	STCA_EMENI	Q12397 emericella
26	49	27.4	750	1	CTPB_MYCLE	P46840 mycobacteri
27	48.5	27.1	901	1	ODP1_MYCTU	Q10504 mycobacteri
28	48	26.8	156	1	YL95_RALSO	Q8xxc0 ralstonia s
29	48	26.8	342	1	HUPK_AZOVI	P31878 azotobacter
30	48	26.8	348	1	HOXV_AZOVI	P40597 azotobacter
31	48	26.8	559	1	ILVD_WOLSU	Q7man4 wolinella s
32	48	26.8	573	1	Y2G8_MYCLE	O33089 mycobacteri
33	48	26.8	833	1	HSF_YEAST	P10961 saccharomyc
34	48	26.8	1122	1	VAB1_CAEEL	O61460 caenorhabdi
35	47.5	26.5	104	1	METJ_ECOLI	P08338 escherichia
36	47.5	26.5	104	1	METJ_SALTY	P06203 salmonella
37	47.5	26.5	306	1	YE86_MYCAV	O07402 mycobacteri
38	47	26.3	275	1	TAUC_ECOLI	Q47539 escherichia
39	46.5	26.0	37	1	DIU1_TENMO	P56618 tenebrio mo
40	46.5	26.0	47	1	DIU2_TENMO	P56619 tenebrio mo
41	46.5	26.0	316	1	VP23_VZVD	P09291 varicella-z
42	46.5	26.0	539	1	STG2_HUMAN	Q9ny99 homo sapien
43	46	25.7	362	1	VI24_YEAST	P38263 saccharomyc
44	46	25.7	413	1	FTSA_BORBU	Q44774 borrelia bu
45	46	25.7	565	1	DEAF_HUMAN	O75398 homo sapien

ALIGNMENTS

RESULT 1
UCN2_MOUSE
ID UCN2_MOUSE STANDARD; PRT; 112 AA.
AC Q99ML8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Urocortin II precursor (Ucn II).
GN UCN2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=21126973; PubMed=11226328;
RA Reyes T.M., Lewis K., Perrin M.H., Kunitake K.S., Vaughan J.,
RA Arias C.A., Hogenesch J.B., Gulyas J., Rivier J., Vale W.W.,
RA Sawchenko P.E.;
RT "Urocortin II: A member of the corticotropin-releasing factor (CRF)
RT neuropeptide family that is selectively bound by type 2 CRF
RT receptors.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:2843-2848(2001).
CC -!- FUNCTION: Suppress food intake, delays gastric emptying and
CC decreases heat-induced edema. Might represent an endogenous ligand
CC for maintaining homeostasis after stress (By similarity).
CC -!- SUBUNIT: Binds with high affinity to CRF receptors 2-alpha and 2-
CC beta (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing
CC factor/urotensin I family.
CC ---

CC ---
DR EMBL; AF331517; AAK16157.1; -.
DR MGD; MGI:2176375; Ucn2.
DR GO; GO:0005576; C:extracellular; ISS.
DR GO; GO:0005102; F:receptor binding; ISS.
DR GO; GO:0006171; P:cAMP biosynthesis; ISS.
DR GO; GO:0007586; P:digestion; ISS.
DR GO; GO:0006950; P:response to stress; ISS.
KW Hormone; Amidation; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 20 70 POTENTIAL.
FT CHAIN 72 112 UROCORTIN II.
SQ SEQUENCE 112 AA; 12179 MW; C871002CDAA64FB7 CRC64;

Query Match 100.0%; Score 179; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 6.2e-19;

```
  Matches   38;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              |||||||||||||||||||||||||||||||||||||||
Db         72 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 109


RESULT 2
UCN2_RAT
ID   UCN2_RAT       STANDARD;      PRT;   109 AA.
AC   Q91WW1;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Urocortin II precursor (Ucn II).
GN   UCN2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Midbrain;
RA   Park J.H., Ju S.K., Lee M.K.;
RT   "Cloning and analysis of tissue-specific mRNA expression of rat
RT   urocortin II.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Suppress food intake, delays gastric emptying and
CC       decreases heat-induced edema. Might represent an endogenous ligand
CC       for maintaining homeostasis after stress (By similarity).
CC   -!- SUBUNIT: Binds with high affinity to CRF receptors 2-alpha and 2-
CC       beta (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing
CC       factor/urotensin I family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AY044835; AAK98780.1; -.
DR   GO; GO:0005576; C:extracellular; ISS.
DR   GO; GO:0005102; F:receptor binding; ISS.
DR   GO; GO:0006171; P:cAMP biosynthesis; ISS.
DR   GO; GO:0007586; P:digestion; ISS.
DR   GO; GO:0006950; P:response to stress; ISS.
DR   InterPro; IPR000187; corticoliberin.
DR   SMART; SM00039; CRF; 1.
KW   Hormone; Amidation; Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   PROPEP       20     67       POTENTIAL.
FT   CHAIN        69    109       UROCORTIN II.
SQ   SEQUENCE   109 AA;  11922 MW;  AA2B46D8903ED83E CRC64;

  Query Match             90.5%;  Score 162;  DB 1;  Length 109;
  Best Local Similarity   94.7%;  Pred. No. 1.8e-16;
  Matches   36;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              |||||||||||||||||||| |||||||||||||||||
Db         69 VILSLDVPIGLLRILLEQARNKAARNQAATNAQILARV 106


RESULT 3
UCN2_HUMAN
ID   UCN2_HUMAN     STANDARD;      PRT;   112 AA.
AC   Q96RP3; Q9BUG0;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Urocortin II precursor (Ucn II) (Stresscopin-related peptide)
DE   (Urocortin-related peptide).
GN   UCN2 OR SRP OR URP.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21227098; PubMed=11329063;
RA   Hsu S.Y., Hsueh A.J.W.;
RT   "Human stresscopin and stresscopin-related peptide are selective
RT   ligands for the type 2 corticotropin-releasing hormone receptor.";
RL   Nat. Med. 7:605-611(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skin, and Uterus;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Suppress food intake, delays gastric emptying and
CC       decreases heat-induced edema. Might represent an endogenous ligand
CC       for maintaining homeostasis after stress.
CC   -!- SUBUNIT: Binds with high affinity to CRF receptors 2-alpha and 2-
CC       beta.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing
CC       factor/urotensin I family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF320560; AAK52672.1; -.
DR   EMBL; BC002647; AAH02647.2; -.
DR   EMBL; BC022096; AAH22096.1; -.
DR   MIM; 605902; -.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0005102; F:receptor binding; IPI.
DR   GO; GO:0006171; P:cAMP biosynthesis; IEP.
DR   GO; GO:0007586; P:digestion; NAS.
DR   GO; GO:0006950; P:response to stress; NAS.
DR   InterPro; IPR000187; corticoliberin.
DR   SMART; SM00039; CRF; 1.
KW   Hormone; Amidation; Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   PROPEP       20     70       POTENTIAL.
FT   CHAIN        72    112       UROCORTIN II.
SQ   SEQUENCE   112 AA;  12146 MW;  0EFF29A3463723D4 CRC64;
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  Query Match             77.7%;  Score 139;  DB 1;  Length 112;
  Best Local Similarity   76.3%;  Pred. No. 4e-13;
  Matches   29;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              ::|||||||||||:|||||||  :||| || |||:||| |
Db         72 IVLSLDVPIGLLQILLEQARARAAREQATTNARILARV 109


RESULT 4
UCN3_HUMAN
ID   UCN3_HUMAN     STANDARD;      PRT;   161 AA.
AC   Q969E3;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Urocortin III precursor (Ucn III) (Stresscopin).
GN   UCN3 OR SPC.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND SYNTHESIS OF UCN III.
RX   MEDLINE=21310014; PubMed=11416224;
RA   Lewis K., Li C., Perrin M.H., Blount A., Kunitake K., Donaldson C.,
RA   Vaughan J., Reyes T.M., Gulyas J., Fischer W., Bilezikjian L.,
RA   Rivier J., Sawchenko P.E., Vale W.W.;
RT   "Identification of urocortin III, an additional member of the
RT   corticotropin-releasing factor (CRF) family with high affinity for the
RT   CRF2 receptor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:7570-7575(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21227098; PubMed=11329063;
RA   Hsu S.Y., Hsueh A.J.W.;
RT   "Human stresscopin and stresscopin-related peptide are selective
RT   ligands for the type 2 corticotropin-releasing hormone receptor.";
RL   Nat. Med. 7:605-611(2001).
CC   -!- FUNCTION: Suppress food intake, delays gastric emptying and
CC       decreases heat-induced edema. Might represent an endogenous ligand
CC       for maintaining homeostasis after stress.
CC   -!- SUBUNIT: Binds with high affinity to CRF receptors 2-alpha and 2-
CC       beta.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing
CC       factor/urotensin I family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF361943; AAK67317.1; -.
DR   EMBL; AY026949; AAK11729.1; -.
DR   Genew; HGNC:17781; UCN3.
DR   MIM; 605901; -.
KW   Hormone; Amidation; Signal.
FT   SIGNAL       1     21       POTENTIAL.
FT   PROPEP      22    118
FT   CHAIN      120    157       UROCORTIN III.
FT   MOD_RES    157    157       AMIDATION (G-158 PROVIDE AMIDE GROUP).
SQ   SEQUENCE   161 AA;  17862 MW;  F92B2C8C3087857D CRC64;

  Query Match             43.6%;  Score 78;  DB 1;  Length 161;
  Best Local Similarity   44.4%;  Pred. No. 0.00042;
  Matches   16;  Conservative    7;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              ||||||  :: :|   |: |  | ||| || ::| :
Db        122 LSLDVPTNIMNLLFNIAKAKNLRAQAAANAHLMAQI 157


RESULT 5
UCN3_MOUSE
ID   UCN3_MOUSE     STANDARD;      PRT;   164 AA.
AC   Q924A4;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Urocortin III precursor (Ucn III).
GN   UCN3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A., SYNTHESIS OF UCN III, AND TISSUE SPECIFICITY.
RX   MEDLINE=21310014; PubMed=11416224;
RA   Lewis K., Li C., Perrin M.H., Blount A., Kunitake K., Donaldson C.,
RA   Vaughan J., Reyes T.M., Gulyas J., Fischer W., Bilezikjian L.,
RA   Rivier J., Sawchenko P.E., Vale W.W.;
RT   "Identification of urocortin III, an additional member of the
RT   corticotropin-releasing factor (CRF) family with high affinity for the
RT   CRF2 receptor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:7570-7575(2001).
CC   -!- FUNCTION: Suppress food intake, delays gastric emptying and
CC       decreases heat-induced edema. Might represent an endogenous ligand
CC       for maintaining homeostasis after stress (By similarity).
CC   -!- SUBUNIT: Binds with high affinity to CRF receptors 2-alpha and 2-
CC       beta.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Expressed in some areas of the brain including
CC       the hypothalamus, amygdala, and brainstem, but is not evident in
CC       the cerebellum, pituitary, or cerebral cortex; it is also
CC       expressed peripherally in small intestine and skin.
CC   -!- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing
CC       factor/urotensin I family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF361944; AAK67318.1; -.
DR   MGD; MGI:1932970; Ucn3.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0007189; P:G-protein signaling, adenylate cyclase acti. . .; IDA.
KW   Hormone; Amidation; Signal.
FT   SIGNAL       1     23       POTENTIAL.
FT   PROPEP      24    121
FT   CHAIN      123    160       UROCORTIN III.
FT   MOD_RES    160    160       AMIDATION (G-161 PROVIDE AMIDE GROUP).
SQ   SEQUENCE   164 AA;  18063 MW;  93A77CB93DA56E5C CRC64;

  Query Match             41.9%;  Score 75;  DB 1;  Length 164;
  Best Local Similarity   44.4%;  Pred. No. 0.0012;
  Matches   16;  Conservative    7;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              ||||||  :: ||    : |  | :|| |||::| :
Db        125 LSLDVPTNIMNILFNIDKAKNLRAKAAANAQLMAQI 160


RESULT 6
UR1_CATCO
ID   UR1_CATCO      STANDARD;      PRT;    41 AA.
AC   P01145;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
```

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DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Urotensin I.
OS   Catostomus commersoni (White sucker).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Catostomidae; Catostomus.
OX   NCBI_TaxID=7971;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=83016606; PubMed=6981844;
RA   Lederis K., Letter A., McMaster D., Moore G., Schlesinger D.;
RT   "Complete amino acid sequence of urotensin I, a hypotensive and
RT   corticotropin-releasing neuropeptide from Catostomus.";
RL   Science 218:162-164(1982).
RN   [2]
RP   SEQUENCE.
RX   MEDLINE=84025881; PubMed=6313156;
RA   Lederis K., Letter A., McMaster D., Ichikawa T., McCannell K.L.,
RA   Rivier J., Rivier C., Vale W., Fryer J., Kobayashi Y.;
RT   "Isolation, analysis of structure, synthesis, and biological actions
RT   of urotensin I neuropeptides.";
RL   Can. J. Biochem. Cell Biol. 61:602-614(1983).
CC   -!- FUNCTION: Urotensin is found in the teleost caudal neurosecretory
CC       system. It has a suggested role in osmoregulation and as a
CC       corticotropin-releasing factor.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing
CC       factor/urotensin I family.
DR   PIR; A94267; UOCC1M.
DR   InterPro; IPR000187; corticoliberin.
DR   InterPro; IPR003620; Urocortin_CRF.
DR   Pfam; PF00473; CRF; 1.
DR   PRINTS; PR01612; CRFFAMILY.
DR   ProDom; PD005970; Urocortin_CRF; 1.
DR   SMART; SM00039; CRF; 1.
DR   PROSITE; PS00511; CRF; 1.
KW   Hormone; Amidation.
FT   MOD_RES      41     41       AMIDATION.
SQ   SEQUENCE   41 AA;  4870 MW;  AEDB309BFB4A1971 CRC64;

  Query Match             34.1%;  Score 61;  DB 1;  Length 41;
  Best Local Similarity   38.9%;  Pred. No. 0.03;
  Matches   14;  Conservative    7;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              :|:|:   ||| ::| || :  | ||  | : | |
Db          6 ISIDLTFHLLRNMIEMARIENEREQAGLNRKYLDEV 41


RESULT 7
UCN1_MOUSE
ID   UCN1_MOUSE     STANDARD;      PRT;   122 AA.
AC   P81615; O88390;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Urocortin precursor.
GN   UCN.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98292491; PubMed=9628819;
RA   Zhao L., Donaldson C.J., Smith G.W., Vale W.W.;
RT   "The structures of the mouse and human urocortin genes.";
RL   Genomics 50:23-33(1998).
CC   -!- FUNCTION: Acts in vitro to stimulate the secretion of
CC       adrenocorticotropic hormone (ACTH). Binds with high affinity to
CC       CRF Receptor types 1, 2-alpha, and 2-beta.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing
CC       factor/urotensin I family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF038632; AAC24202.1; -.
DR   MGD; MGI:1276123; Ucn.
DR   InterPro; IPR000187; corticoliberin.
DR   InterPro; IPR003620; Urocortin_CRF.
DR   Pfam; PF00473; CRF; 1.
DR   PRINTS; PR01612; CRFFAMILY.
DR   SMART; SM00039; CRF; 1.
DR   PROSITE; PS00511; CRF; 1.
KW   Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT   SIGNAL       1     25       POTENTIAL.
FT   PROPEP      26     80       BY SIMILARITY.
FT   PEPTIDE     81    120       UROCORTIN.
FT   MOD_RES     120   120       AMIDATION (G-121 PROVIDE AMIDE GROUP) (BY
FT                               SIMILARITY).
SQ   SEQUENCE   122 AA;  13557 MW;  D2969756F36F5DEA CRC64;

  Query Match             33.5%;  Score 60;  DB 1;  Length 122;
  Best Local Similarity   44.4%;  Pred. No. 0.13;
  Matches   16;  Conservative    5;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              ||:|:   ||| ||| || :: | :|  |  |   |
Db         85 LSIDLTFHLLRTLLELARTQSQRERAEQNRIIFDSV 120


RESULT 8
UCN1_RAT
ID   UCN1_RAT       STANDARD;      PRT;   122 AA.
AC   P55090;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Urocortin precursor (Corticotensin).
GN   UCN.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=96069764; PubMed=7477349;
RA   Vaughan J.M., Donaldson C.J., Bittencourt J., Perrin M.H., Lewis K.A.,
RA   Sutton S.W., Chan R., Turnbull A., Lovejoy D., Rivier C., Rivier J.E.,
RA   Sawchenko P., Vale W.W.;
RT   "Urocortin, a mammalian neuropeptide related to fish urotensin I and
RT   to corticotropin-releasing factor.";
RL   Nature 378:287-292(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Lewis;
RA   Park J.H., Lee Y.J., Kim K.L.;
RT   "Detection of rat urocortin in lymphoid tissues: implications for the
RT   functional assessment of urocortin as a novel neuro-immunomodulatory
RT   peptide.";
RL   Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Acts in vitro to stimulate the secretion of
CC       adrenocorticotropic hormone (ACTH). Binds with high affinity to
CC       CRF Receptor types 1, 2-alpha, and 2-beta.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing
CC       factor/urotensin I family.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; U33935; AAA87566.1; -.
DR   EMBL; AF093623; AAF63153.1; -.
DR   PIR; S60262; S60262.
DR   InterPro; IPR000187; corticoliberin.
DR   InterPro; IPR003620; Urocortin_CRF.
DR   Pfam; PF00473; CRF; 1.
DR   PRINTS; PR01612; CRFFAMILY.
DR   SMART; SM00039; CRF; 1.
DR   PROSITE; PS00511; CRF; 1.
KW   Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT   SIGNAL        1     25       POTENTIAL.
FT   PROPEP       26     80
FT   PEPTIDE      81    120       UROCORTIN.
FT   MOD_RES     120    120       AMIDATION (G-121 PROVIDE AMIDE GROUP) (BY
FT                                SIMILARITY).
SQ   SEQUENCE   122 AA;  13711 MW;  9F0AF834CBFFCE74 CRC64;

  Query Match             33.5%;  Score 60;  DB 1;  Length 122;
  Best Local Similarity   44.4%;  Pred. No. 0.13;
  Matches   16;  Conservative    5;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              ||:|:   ||| ||| || :: | :|  |  |   |
Db         85 LSIDLTFHLLRTLLELARTQSQRERAEQNRIIFDSV 120


RESULT 9
UCN1_HUMAN
ID   UCN1_HUMAN     STANDARD;      PRT;   124 AA.
AC   P55089;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Urocortin precursor.
GN   UCN.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=96198824; PubMed=8612563;
RA   Donaldson C.J., Sutton S.W., Perrin M.H., Corrigan A.Z., Lewis K.A.,
RA   Rivier J.E., Vaughan J.M., Vale W.W.;
RT   "Cloning and characterization of human urocortin.";
RL   Endocrinology 137:2167-2170(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98292491; PubMed=9628819;
RA   Zhao L., Donaldson C.J., Smith G.W., Vale W.W.;
RT   "The structures of the mouse and human urocortin genes.";
RL   Genomics 50:23-33(1998).
CC   -!- FUNCTION: Acts in vitro to stimulate the secretion of
CC       adrenocorticotropic hormone (ACTH). Binds with high affinity to
CC       CRF Receptor types 1, 2-alpha, and 2-beta.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing
CC       factor/urotensin I family.
CC   ---------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; AF038633; AAC24204.1; -.
DR   Genew; HGNC:12516; UCN.
DR   MIM; 600945; -.
DR   GO; GO:0005184; F:neuropeptide hormone activity; TAS.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR   InterPro; IPR000187; corticoliberin.
DR   InterPro; IPR003620; Urocortin_CRF.
DR   Pfam; PF00473; CRF; 1.
DR   PRINTS; PR01612; CRFFAMILY.
DR   SMART; SM00039; CRF; 1.
DR   PROSITE; PS00511; CRF; 1.
KW   Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT   SIGNAL        1     25       POTENTIAL.
FT   PROPEP       26     82
FT   PEPTIDE      83    122       UROCORTIN.
FT   MOD_RES     122    122       AMIDATION (G-123 PROVIDE AMIDE GROUP) (BY
FT                                SIMILARITY).
SQ   SEQUENCE   124 AA;  13458 MW;  4F765DA75DDD4A5E CRC64;

  Query Match             33.5%;  Score 60;  DB 1;  Length 124;
  Best Local Similarity   44.4%;  Pred. No. 0.13;
  Matches   16;  Conservative    5;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              ||:|:   ||| ||| || :: | :|  |  |   |
Db         87 LSIDLTFHLLRTLLELARTQSQRERAEQNRIIFDSV 122


RESULT 10
UR1_CARAU
ID   UR1_CARAU      STANDARD;      PRT;   145 AA.
AC   Q9PTQ4;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Urotensin I precursor.
OS   Carassius auratus (Goldfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Carassius.
OX   NCBI_TaxID=7957;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=20072640; PubMed=10603283;
RA   Bernier N.J., Lin X., Peter R.E.;
RT   "Differential expression of corticotropin-releasing factor (CRF) and
RT   urotensin I precursor genes, and evidence of CRF gene expression
RT   regulated by cortisol in goldfish brain.";
RL   Gen. Comp. Endocrinol. 116:461-477(1999).
CC   -!- FUNCTION: Urotensin is found in the teleost caudal neurosecretory
CC       system. It has a suggested role in osmoregulation and as a
CC       corticotropin-releasing factor. The nonhormonal portion of this
CC       precursor may be a urotensin binding protein, urophysin.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing
CC       factor/urotensin I family.
CC   ---------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; AF129115; AAF24136.1; -.
DR   InterPro; IPR000187; corticoliberin.
DR   InterPro; IPR003620; Urocortin_CRF.
DR   Pfam; PF00473; CRF; 1.
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DR   PRINTS; PR01612; CRFFAMILY.
DR   ProDom; PD005970; Urocortin_CRF; 1.
DR   SMART; SM00039; CRF; 1.
DR   PROSITE; PS00511; CRF; 1.
KW   Hormone; Cleavage on pair of basic residues; Amidation; Signal.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23    100       UROPHYSIN (POTENTIAL).
FT   PEPTIDE     103    143       UROTENSIN I.
FT   MOD_RES     143    143       AMIDATION (G-144 PROVIDE AMIDE GROUP) (BY
FT                                SIMILARITY).
SQ   SEQUENCE   145 AA;  16241 MW;  5836B3E41A062E71 CRC64;

  Query Match             33.5%;  Score 60;  DB 1;  Length 145;
  Best Local Similarity   38.9%;  Pred. No. 0.16;
  Matches   14;  Conservative    7;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              :|:|:   ||| ::| || :  | ||  | : |  |
Db        108 ISIDLTFHLLRNMIEMARNENQREQAGLNRKYLDEV 143


RESULT 11
UR1_CYPCA
ID   UR1_CYPCA      STANDARD;      PRT;   145 AA.
AC   P01146;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Urotensin I precursor.
OS   Cyprinus carpio (Common carp).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Cyprinus.
OX   NCBI_TaxID=7962;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86094380; PubMed=3484550;
RA   Ishida I., Ichikawa T., Deguchi T.;
RT   "Cloning and sequence analysis of cDNA encoding urotensin I
RT   precursor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 83:308-312(1986).
RN   [2]
RP   SEQUENCE OF 103-143.
RX   MEDLINE=83090718; PubMed=6757895;
RA   Ichikawa T., McMaster D., Lederis K., Kobayashi H.;
RT   "Isolation and amino acid sequence of urotensin I, a vasoactive and
RT   ACTH-releasing neuropeptide, from the carp (Cyprinus carpio)
RT   urophysis.";
RL   Peptides 3:859-867(1982).
RN   [3]
RP   SEQUENCE OF 103-143, AND SYNTHESIS OF 103-143.
RX   MEDLINE=84025881; PubMed=6313156;
RA   Lederis K., Letter A., McMaster D., Ichikawa T., McCannell K.L.,
RA   Rivier J., Rivier C., Vale W., Fryer J., Kobayashi Y.;
RT   "Isolation, analysis of structure, synthesis, and biological actions
RT   of urotensin I neuropeptides.";
RL   Can. J. Biochem. Cell Biol. 61:602-614(1983).
CC   -!- FUNCTION: Urotensin is found in the teleost caudal neurosecretory
CC       system. It has a suggested role in osmoregulation and as a
CC       corticotropin-releasing factor. The nonhormonal portion of this
CC       precursor may be a urotensin binding protein, urophysin.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing
CC       factor/urotensin I family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M11671; AAA49214.1; -.
DR   PIR; A94096; UOCA1.
DR   InterPro; IPR000187; corticoliberin.
DR   InterPro; IPR003620; Urocortin_CRF.
DR   Pfam; PF00473; CRF; 1.
DR   PRINTS; PR01612; CRFFAMILY.
DR   ProDom; PD005970; Urocortin_CRF; 1.
DR   SMART; SM00039; CRF; 1.
DR   PROSITE; PS00511; CRF; 1.
KW   Hormone; Cleavage on pair of basic residues; Amidation; Signal.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23    100       UROPHYSIN (POTENTIAL).
FT   PEPTIDE     103    143       UROTENSIN I.
FT   MOD_RES     143    143       AMIDATION (G-144 PROVIDE AMIDE GROUP).
SQ   SEQUENCE   145 AA;  16249 MW;  4F16166A580E20FB CRC64;

  Query Match             33.5%;  Score 60;  DB 1;  Length 145;
  Best Local Similarity   38.9%;  Pred. No. 0.16;
  Matches   14;  Conservative    7;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              :|:|:   ||| ::| || :  | ||  | : |  |
Db        108 ISIDLTFHLLRNMIEMARNENQREQAGLNRKYLDEV 143


RESULT 12
UR1_ONCMY
ID   UR1_ONCMY      STANDARD;      PRT;   165 AA.
AC   O93448;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Urotensin I precursor.
OS   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX   NCBI_TaxID=8022;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Hypothalamus;
RX   MEDLINE=99348219; PubMed=10417230;
RA   Barsyte D., Tipping D.R., Smart D., Conlon J.M., Baker B.I.,
RA   Lovejoy D.A.;
RT   "Rainbow trout (Oncorhynchus mykiss) urotensin-I: structural
RT   differences between urotensins-I and urocortins.";
RL   Gen. Comp. Endocrinol. 115:169-177(1999).
CC   -!- FUNCTION: Urotensin is found in the teleost caudal neurosecretory
CC       system. It has a suggested role in osmoregulation and as a
CC       corticotropin-releasing factor. The nonhormonal portion of this
CC       precursor may be a urotensin binding protein, urophysin.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing
CC       factor/urotensin I family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ005264; CAA06461.1; -.
DR   InterPro; IPR000187; corticoliberin.
DR   InterPro; IPR003620; Urocortin_CRF.
DR   Pfam; PF00473; CRF; 1.
DR   PRINTS; PR01612; CRFFAMILY.
DR   ProDom; PD005970; Urocortin_CRF; 1.
DR   SMART; SM00039; CRF; 1.
DR   PROSITE; PS00511; CRF; 1.
KW   Hormone; Cleavage on pair of basic residues; Amidation; Signal.
FT   SIGNAL        1     18       POTENTIAL.
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FT   CHAIN        19    120       UROPHYSIN (POTENTIAL).
FT   PEPTIDE     123    163       UROTENSIN-I.
FT   MOD_RES     163    163       AMIDATION (G-164 PROVIDE AMIDE GROUP) (BY
FT                                SIMILARITY).
SQ   SEQUENCE   165 AA;  18631 MW;  3263357EE76E3A1A CRC64;

  Query Match             33.5%;  Score 60;  DB 1;  Length 165;
  Best Local Similarity   36.1%;  Pred. No. 0.18;
  Matches   13;  Conservative    9;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              :|:|:   ||| ::| || :: : ||  | : | |
Db        128 ISIDLTFHLLRNMIEMARIESQKEQAELNRKYLDEV 163


RESULT 13
CRF_XENLA
ID   CRF_XENLA      STANDARD;      PRT;   162 AA.
AC   P49188;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Corticoliberin precursor (Corticotropin-releasing factor) (CRF)
DE   (Corticotropin releasing hormone).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93078805; PubMed=1448118;
RA   Stenzel-Poore M.P., Heldwein K.A., Stenzel P., Lee S., Vale W.W.;
RT   "Characterization of the genomic corticotropin-releasing factor (CRF)
RT   gene from Xenopus laevis: two members of the CRF family exist in
RT   amphibians.";
RL   Mol. Endocrinol. 6:1716-1724(1992).
CC   -!- FUNCTION: This hormone from hypothalamus regulates the release of
CC       corticotropin from pituitary gland (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing
CC       factor/urotensin I family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; S50096; AAB24277.1; -.
DR   PIR; A45362; A45362.
DR   InterPro; IPR000187; corticoliberin.
DR   InterPro; IPR003620; Urocortin_CRF.
DR   Pfam; PF00473; CRF; 1.
DR   PRINTS; PR01612; CRFFAMILY.
DR   ProDom; PD005970; Urocortin_CRF; 1.
DR   SMART; SM00039; CRF; 1.
DR   PROSITE; PS00511; CRF; 1.
KW   Hormone; Amidation; Hypothalamus; Cleavage on pair of basic residues;
KW   Signal.
FT   SIGNAL        1     24       POTENTIAL.
FT   PROPEP       25    119
FT   PEPTIDE     120    160       CORTICOLIBERIN.
FT   MOD_RES     160    160       AMIDATION (G-161 PROVIDE AMIDE GROUP).
SQ   SEQUENCE   162 AA;  17880 MW;  02E6906ACA0636CB CRC64;

  Query Match             31.8%;  Score 57;  DB 1;  Length 162;
  Best Local Similarity   39.4%;  Pred. No. 0.48;
  Matches   13;  Conservative    8;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQIL 35
              :|||:   ||| :|| || :    || :| :::
Db        125 ISLDLTFHLLREVLEMARAEQIAQQAHSNRKLM 157


RESULT 14
CRF_RAT
ID   CRF_RAT        STANDARD;      PRT;   187 AA.
AC   P01143;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Corticoliberin precursor (Corticotropin-releasing factor) (CRF)
DE   (Corticotropin releasing hormone).
GN   CRH.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86030658; PubMed=3876950;
RA   Jingami H., Mizuno N., Takahashi H., Shibahara S., Furutani Y.,
RA   Imura H., Numa S.;
RT   "Cloning and sequence analysis of cDNA for rat
RT   corticotropin-releasing factor precursor.";
RL   FEBS Lett. 191:63-66(1985).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=90331928; PubMed=3274895;
RA   Thompson R.C., Seasholtz A.F., Herbert E.;
RT   "Rat corticotropin-releasing hormone gene: sequence and
RT   tissue-specific expression.";
RL   Mol. Endocrinol. 1:363-370(1987).
RN   [3]
RP   SEQUENCE OF 145-185.
RX   MEDLINE=83273710; PubMed=6603620;
RA   Rivier J., Spiess J., Vale W.;
RT   "Characterization of rat hypothalamic corticotropin-releasing
RT   factor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:4851-4855(1983).
CC   -!- FUNCTION: This hormone from hypothalamus regulates the release of
CC       corticotropin from pituitary gland.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing
CC       factor/urotensin I family.
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CC   ---------------------------------------------------------------------
DR   EMBL; X03036; CAA26838.1; -.
DR   EMBL; M54987; AAA40965.1; -.
DR   PIR; A40906; RHRTCE.
DR   InterPro; IPR000187; corticoliberin.
DR   InterPro; IPR003620; Urocortin_CRF.
DR   Pfam; PF00473; CRF; 1.
DR   PRINTS; PR01612; CRFFAMILY.
DR   ProDom; PD005970; Urocortin_CRF; 1.
DR   SMART; SM00039; CRF; 1.
DR   PROSITE; PS00511; CRF; 1.
KW   Hormone; Amidation; Hypothalamus; Cleavage on pair of basic residues;
KW   Signal.
FT   SIGNAL        1     24       PROBABLE.
FT   PROPEP       25    144
FT   PEPTIDE     145    185       CORTICOLIBERIN.
FT   MOD_RES     185    185       AMIDATION (G-186 PROVIDE AMIDE GROUP).
SQ   SEQUENCE   187 AA;  20680 MW;  911602C82A444CFB CRC64;
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  Query Match             31.8%;  Score 57;  DB 1;  Length 187;
  Best Local Similarity   39.4%;  Pred. No. 0.56;
  Matches   13;  Conservative    8;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQIL 35
              :|||:   ||| :|| || :    || :| :::
Db        150 ISLDLTFHLLREVLEMARAEQLAQQAHSNRKLM 182


RESULT 15
CRF_PIG
ID   CRF_PIG        STANDARD;      PRT;   191 AA.
AC   P06296; O62637;
DT   01-JAN-1988 (Rel. 06, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Corticoliberin precursor (Corticotropin-releasing factor) (CRF)
DE   (Corticotropin releasing hormone).
GN   CRH.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98403942; PubMed=9734873;
RA   Mimmack M.L., Parrott R.F., Vellucci S.V.;
RT   "Molecular cloning of the porcine corticotropin-releasing factor
RT   gene.";
RL   J. Anim. Sci. 76:2205-2206(1998).
RN   [2]
RP   SEQUENCE OF 149-189.
RX   MEDLINE=86094305; PubMed=3878520;
RA   Patthy M., Horvath J., Mason-Garcia M., Szoke B., Schlesinger D.H.,
RA   Schally A.V.;
RT   "Isolation and amino acid sequence of corticotropin-releasing factor
RT   from pig hypothalami.";
RL   Proc. Natl. Acad. Sci. U.S.A. 82:8762-8766(1985).
CC   -!- FUNCTION: This hormone from hypothalamus regulates the release of
CC       corticotropin from pituitary gland.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing
CC       factor/urotensin I family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y15159; CAA75424.1; -.
DR   PIR; A01404; RHPGCE.
DR   InterPro; IPR000187; corticoliberin.
DR   InterPro; IPR003620; Urocortin_CRF.
DR   Pfam; PF00473; CRF; 1.
DR   PRINTS; PR01612; CRFFAMILY.
DR   ProDom; PD005970; Urocortin_CRF; 1.
DR   SMART; SM00039; CRF; 1.
DR   PROSITE; PS00511; CRF; 1.
KW   Hormone; Amidation; Hypothalamus; Cleavage on pair of basic residues;
KW   Signal.
FT   SIGNAL        1     24       PROBABLE.
FT   PROPEP       25    148
FT   PEPTIDE     149    189       CORTICOLIBERIN.
FT   MOD_RES     189    189       AMIDATION (G-190 PROVIDE AMIDE GROUP).
FT   CONFLICT    188    188       I -> F (IN REF. 2).
SQ   SEQUENCE   191 AA;  21042 MW;  166513C1CEDC9B7D CRC64;

  Query Match             31.8%;  Score 57;  DB 1;  Length 191;
  Best Local Similarity   39.4%;  Pred. No. 0.57;
  Matches   13;  Conservative    8;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQIL 35
              :|||:   ||| :|| || :    || :| :::
Db        154 ISLDLTFHLLREVLEMARAEQLAQQAHSNRKLM 186


Search completed: April 20, 2004, 18:55:22
Job time : 6.06667 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 20, 2004, 18:52:07 ; Search time 6.84 Seconds
(without alignments)
534.397 Million cell updates/sec

Title: US-09-919-473-11
Perfect score: 179
Sequence: 1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	61	34.1	41	1	UOCC1M	urotensin I - whit
2	60	33.5	122	2	S60262	corticotensin - ra
3	60	33.5	145	1	UOCA1	urotensin I precur
4	57	31.8	41	1	RHPGCE	corticoliberin - p
5	57	31.8	162	2	A45362	corticoliberin pre
6	57	31.8	187	1	RHRTCE	corticoliberin pre
7	57	31.8	196	2	A30327	corticoliberin pre
8	56	31.3	162	2	A31343	corticoliberin 1 p
9	54	30.2	41	2	A43978	urotensin I - Euro
10	54	30.2	162	2	S14597	corticoliberin 2 p
11	53	29.6	40	1	SWFGS	sauvagine - Sauvag
12	52	29.1	393	2	T04957	hypothetical prote
13	51	28.5	412	2	F87709	DNA/pantothenate m
14	50.5	28.2	1325	2	T01037	hypothetical prote
15	50	27.9	159	2	AB1557	methylated-DNA-pro
16	50	27.9	190	1	RHSHCE	corticoliberin pre
17	50	27.9	410	2	AG2693	large terminase [i
18	50	27.9	419	2	D97475	probable large ter
19	50	27.9	875	2	T43522	condensin complex
20	49.5	27.7	288	2	AE1608	phosphotransbutyry
21	49.5	27.7	639	2	T16648	hypothetical prote
22	49	27.4	214	2	AH0265	probable membrane
23	49	27.4	462	2	G83000	probable two-compo
24	49	27.4	750	2	C87159	cation-transportin
25	49	27.4	750	2	S77653	cation-transportin
26	48.5	27.1	238	2	AH0106	hypothetical prote
27	48.5	27.1	901	2	E70778	probable aceE prot
28	48	26.8	239	2	C83637	probable ATP-bindi
29	48	26.8	270	2	B75581	probable cytochrom
30	48	26.8	278	2	D83080	hypothetical prote
31	48	26.8	342	2	S23438	hypothetical prote
32	48	26.8	442	2	A71433	hypothetical prote
33	48	26.8	450	2	C75316	conserved hypothet
34	48	26.8	492	2	T26936	hypothetical prote
35	48	26.8	573	2	T10037	hypothetical prote
36	48	26.8	585	2	A84346	subtilisin homolog
37	48	26.8	772	2	T25469	hypothetical prote
38	48	26.8	833	1	A31593	heat shock transcr
39	48	26.8	919	2	T29581	hypothetical prote
40	48	26.8	1033	2	A96714	hypothetical prote
41	48	26.8	1122	2	T42400	Eph receptor tyros
42	47.5	26.5	105	1	RGECMJ	Met regulon regula
43	47.5	26.5	105	2	A23081	regulatory protein
44	47.5	26.5	105	2	C91237	repressor protein
45	47.5	26.5	105	2	G86084	repressor of all m

ALIGNMENTS

RESULT 1
UOCC1M
urotensin I - white sucker
C;Species: Catostomus commersoni (white sucker)
C;Date: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change 21-Jan-2000
C;Accession: A94267; A90754; A01407
R;Lederis, K.; Letter, A.; McMaster, D.; Moore, G.; Schlesinger, D.
Science 218, 162-164, 1982
A;Title: Complete amino acid sequence of urotensin I, a hypotensive and corticotropin-rel
A;Reference number: A94267; MUID:83016606; PMID:6981844
A;Accession: A94267
A;Molecule type: protein
A;Residues: 1-41 <LE1>
R;Lederis, K.; Letter, A.; McMaster, D.; Ichikawa, T.; MacCannell, K.L.; Rivier, J.; Rivi
Can. J. Biochem. Cell Biol. 61, 602-614, 1983
A;Title: Isolation, analysis of structure, synthesis, and biological actions of urotensir
A;Reference number: A90754; MUID:84025881; PMID:6313156
A;Accession: A90754
A;Molecule type: protein
A;Residues: 1-41 <LE2>
C;Comment: Urotensin I is found in the teleost caudal neurosecretory system and is involv
C;Superfamily: corticoliberin-endorpholiberin; diuretic hormone homology
C;Keywords: amidated carboxyl end; hormone; osmoregulation
F;1-41/Domain: diuretic hormone homology <DHH>
F;41/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 34.1%; Score 61; DB 1; Length 41;
Best Local Similarity 38.9%; Pred. No. 0.041;
Matches 14; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

```
Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              :|:|:   ||| ::| || :  | ||  | : | |
Db          6 ISIDLTFHLLRNMIEMARIENEREQAGLNRKYLDEV 41
```

RESULT 2
S60262
corticotensin - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jan-2003
C;Accession: S60262
R;Vaughan, J.; Donaldson, C.; Bittencourt, J.; Perrin, M.H.; Lewis, K.; Sutton, S.; Chan,
Nature 378, 287-292, 1995
A;Title: Urocortin, a mammalian neuropeptide related to fish urotensin I and to corticotr
A;Reference number: S60262; MUID:96069764; PMID:7477349
A;Accession: S60262
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-122 <VAU>
A;Cross-references: EMBL:U33935; NID:g1065908; PIDN:AAA87566.1; PID:g1065909
C;Superfamily: corticoliberin-endorpholiberin; diuretic hormone homology
F;80-120/Domain: diuretic hormone homology <DHH>

```
  Query Match             33.5%;  Score 60;  DB 2;  Length 122;
  Best Local Similarity   44.4%;  Pred. No. 0.2;
  Matches   16;  Conservative    5;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              ||:|:   ||| ||| || :: | :|  |  |   |
Db         85 LSIDLTFHLLRTLLELARTQSQRERAEQNRIIFDSV 120


RESULT 3
UOCA1
urotensin I precursor - common carp
N;Contains: urotensin I
C;Species: Cyprinus carpio (common carp)
C;Date: 05-Apr-1983 #sequence_revision 31-Mar-1988 #text_change 20-Apr-2001
C;Accession: A94096; A93752; A01408; A25966
R;Ishida, I.; Ichikawa, T.; Deguchi, T.
Proc. Natl. Acad. Sci. U.S.A. 83, 308-312, 1986
A;Title: Cloning and sequence analysis of cDNA encoding urotensin I precursor.
A;Reference number: A94096; MUID:86094380; PMID:3484550
A;Accession: A94096
A;Molecule type: mRNA
A;Residues: 1-145 <ISH>
A;Cross-references: GB:M11671; NID:g213064; PIDN:AAA49214.1; PID:g213065
A;Experimental source: spinal cord
R;Ichikawa, T.; McMaster, D.; Lederis, K.; Kobayashi, H.
Peptides 3, 859-867, 1982
A;Title: Isolation and amino acid sequence of urotensin I, a vasoactive and ACTH-releasi
A;Reference number: A93752; MUID:83090718; PMID:6757895
A;Accession: A93752
A;Molecule type: protein
A;Residues: 103-143 <ICH>
C;Comment: Urotensin I is found in the teleost caudal neurosecretory system. It has a su
C;Comment: The nonhormonal portion of this precursor may be a urotensin binding protein,
C;Superfamily: corticoliberin-endorpholiberin; diuretic hormone homology
C;Keywords: amidated carboxyl end; hormone; osmoregulation
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-145/Product: prourotensin I #status predicted <PRO>
F;103-143/Product: urotensin I #status experimental <MAT>
F;103-143/Domain: diuretic hormone homology <DHH>
F;143/Modified site: amidated carboxyl end (Val) (amide in mature form from following gl

  Query Match             33.5%;  Score 60;  DB 1;  Length 145;
  Best Local Similarity   38.9%;  Pred. No. 0.24;
  Matches   14;  Conservative    7;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              :|:|:   ||| ::| || :  | ||  | : |  |
Db        108 ISIDLTFHLLRNMIEMARNENQREQAGLNRKYLDEV 143


RESULT 4
RHPGCE
corticoliberin - pig
N;Alternate names: corticotropin-releasing factor; CRF; endorpholiberin
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 11-Apr-1997
C;Accession: A01404
R;Patthy, M.; Horvath, J.; Mason-Garcia, M.; Szoke, B.; Schlesinger, D.H.; Schally, A.V.
Proc. Natl. Acad. Sci. U.S.A. 82, 8762-8766, 1985
A;Title: Isolation and amino acid sequence of corticotropin-releasing factor from pig hy
A;Reference number: A01404; MUID:86094305; PMID:3878520
A;Accession: A01404
A;Molecule type: protein
A;Residues: 1-41 <PAT>
A;Note: 40-Ile was also found
C;Comment: This hormone from hypothalamus regulates the release of corticotropin from pi
C;Superfamily: corticoliberin-endorpholiberin; diuretic hormone homology
C;Keywords: amidated carboxyl end; hormone; hypothalamus
F;41/Modified site: amidated carboxyl end (Phe) #status experimental

  Query Match             31.8%;  Score 57;  DB 1;  Length 41;
  Best Local Similarity   39.4%;  Pred. No. 0.16;
  Matches   13;  Conservative    8;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQIL 35
              :|||:   ||| :|| || :    || :| :::
Db          6 ISLDLTFHLLREVLEMARAEQLAQQAHSNRKLM 38


RESULT 5
A45362
corticoliberin precursor - African clawed frog
N;Alternate names: corticotropin-releasing factor
C;Species: Xenopus laevis (African clawed frog)
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999
C;Accession: A45362
R;Stenzel-Poore, M.P.; Heldwein, K.A.; Stenzel, P.; Lee, S.; Vale, W.W.
Mol. Endocrinol. 6, 1716-1724, 1992
A;Title: Characterization of the genomic corticotropin-releasing factor (CRF) gene from
A;Reference number: A45362; MUID:93078805; PMID:1448118
A;Accession: A45362
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-162 <STE>
A;Cross-references: GB:S50096; NID:g260494; PIDN:AAB24277.1; PID:g260495
A;Note: sequence extracted from NCBI backbone (NCBIP:118818)
C;Genetics:
A;Gene: CRF
C;Superfamily: corticoliberin-endorpholiberin; diuretic hormone homology
C;Keywords: amidated carboxyl end; hormone; hypothalamus
F;120-160/Domain: diuretic hormone homology <DHH>

  Query Match             31.8%;  Score 57;  DB 2;  Length 162;
  Best Local Similarity   39.4%;  Pred. No. 0.75;
  Matches   13;  Conservative    8;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQIL 35
              :|||:   ||| :|| || :    || :| :::
Db        125 ISLDLTFHLLREVLEMARAEQIAQQAHSNRKLM 157


RESULT 6
RHRTCE
corticoliberin precursor - rat
N;Alternate names: corticotropin-releasing factor; prepro-CRF
N;Contains: corticoliberin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 14-Nov-1983 #sequence_revision 30-Sep-1987 #text_change 18-Jun-1999
C;Accession: A40906; A91351; A93965; A01405; A24009
R;Thompson, R.C.; Seasholtz, A.F.; Herbert, E.
Mol. Endocrinol. 1, 363-370, 1987
A;Title: Rat corticotropin-releasing hormone gene: sequence and tissue-specific expressic
A;Reference number: A40906; MUID:90331928; PMID:3274895
A;Accession: A40906
A;Molecule type: DNA
A;Residues: 1-187 <THO>
A;Cross-references: GB:M54987; NID:g203593; PIDN:AAA40965.1; PID:g203594
R;Jingami, H.; Mizuno, N.; Takahashi, H.; Shibahara, S.; Furutani, Y.; Imura, H.; Numa,
FEBS Lett. 191, 63-66, 1985
A;Title: Cloning and sequence analysis of cDNA for rat corticotropin-releasing factor pre
A;Reference number: A91351; MUID:86030658; PMID:3876950
A;Accession: A91351
A;Molecule type: mRNA
A;Residues: 1-187 <JIN>
A;Cross-references: GB:X03036; NID:g56008; PIDN:CAA26838.1; PID:g56009
R;Rivier, J.; Spiess, J.; Vale, W.
Proc. Natl. Acad. Sci. U.S.A. 80, 4851-4855, 1983
A;Title: Characterization of rat hypothalamic corticotropin-releasing factor.
A;Reference number: A93965; MUID:83273710; PMID:6603620
A;Accession: A93965
A;Molecule type: protein
A;Residues: 145-185 <RIV>
C;Comment: Corticoliberin from hypothalamus stimulates the release of corticotropin (ACTH
tary gland, testis, spinal cord, and adrenal gland.
```

C;Genetics:
A;Gene: CRH
A;Introns: #status absent
A;Note: one intron is in 5' noncoding region
C;Superfamily: corticoliberin-endorpholiberin; diuretic hormone homology
C;Keywords: amidated carboxyl end; hormone; hypothalamus
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-187/Product: procorticoliberin #status predicted <MAT>
F;145-185/Product: corticoliberin #status experimental <CLN>
F;145-184/Domain: diuretic hormone homology <DHH>
F;185/Modified site: amidated carboxyl end (Ile) (amide in mature form from following gl

Query Match 31.8%; Score 57; DB 1; Length 187;
Best Local Similarity 39.4%; Pred. No. 0.88;
Matches 13; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Qy 3 LSLDVPIGLLRILLEQARYKAARNQAATNAQIL 35
:|||: ||| :|| || : || :| :::
Db 150 ISLDLTFHLLREVLEMARAEQLAQQAHSNRKLM 182

RESULT 7
A30327
corticoliberin precursor - human
N;Alternate names: corticotropin-releasing factor
N;Contains: corticoliberin
C;Species: Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Jul-1999
C;Accession: A30327; A60860; I38106
R;Robinson, B.G.; D'Angio Jr., L.A.; Pasieka, K.B.; Majzoub, J.A.
Mol. Cell. Endocrinol. 61, 175-180, 1989
A;Title: Preprocorticotropin releasing hormone: cDNA sequence and in vitro processing.
A;Reference number: A30327; MUID:89137721; PMID:2783917
A;Accession: A30327
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-196 <ROB>
R;Sasaki, A.; Tempst, P.; Liotta, A.S.; Margioris, A.N.; Hood, L.E.; Kent, S.B.H.; Sato,
J. Clin. Endocrinol. Metab. 67, 768-773, 1988
A;Title: Isolation and characterization of a corticotropin-releasing hormone-like peptid
A;Reference number: A60860; MUID:88331316; PMID:3262120
A;Accession: A60860
A;Molecule type: protein
A;Residues: 154-168,'X',170-186 <SAS>
R;Shibahara, S.; Morimoto, Y.; Furutani, Y.; Notake, M.; Takahashi, H.; Shimizu, S.; Hor
EMBO J. 2, 775-779, 1983
A;Title: Isolation and sequence analysis of the human corticotropin-releasing factor pre
A;Reference number: I38106; MUID:84057755; PMID:6605851
A;Accession: I38106
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-196 <RES>
A;Cross-references: EMBL:V00571; NID:g35355; PIDN:CAA23834.1; PID:g35356
C;Genetics:
A;Gene: GDB:CRH
A;Cross-references: GDB:119804; OMIM:122560
A;Map position: 8q13-8q13
C;Superfamily: corticoliberin-endorpholiberin; diuretic hormone homology
C;Keywords: amidated carboxyl end; hormone; hypothalamus; placenta
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-196/Product: procorticoliberin #status predicted <MAT>
F;154-194/Product: corticoliberin #status predicted <CLN>
F;154-193/Domain: diuretic hormone homology <DHH>
F;194/Modified site: amidated carboxyl end (Ile) (amide in mature form from following gl

Query Match 31.8%; Score 57; DB 2; Length 196;
Best Local Similarity 39.4%; Pred. No. 0.93;
Matches 13; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Qy 3 LSLDVPIGLLRILLEQARYKAARNQAATNAQIL 35
:|||: ||| :|| || : || :| :::
Db 159 ISLDLTFHLLREVLEMARAEQLAQQAHSNRKLM 191

RESULT 8
A31343
corticoliberin 1 precursor - white sucker
N;Contains: corticoliberin 1
C;Species: Catostomus commersoni (white sucker)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 16-Jul-1999
C;Accession: A31343
R;Okawara, Y.; Morley, S.D.; Burzio, L.O.; Zwiers, H.; Lederis, K.; Richter, D.
Proc. Natl. Acad. Sci. U.S.A. 85, 8439-8443, 1988
A;Title: Cloning and sequence analysis of cDNA for corticotropin-releasing factor precurs
A;Reference number: A31343; MUID:89042199; PMID:3186733
A;Accession: A31343
A;Molecule type: mRNA
A;Residues: 1-162 <OKA>
A;Cross-references: GB:J04116; NID:g156135; PIDN:AAA81529.1; PID:g156136
C;Superfamily: corticoliberin-endorpholiberin; diuretic hormone homology
C;Keywords: amidated carboxyl end; hormone
F;1-24/Domain: (or 1-27 or 1-28 or 1-29) signal sequence #status predicted <SIG>
F;25-162/Product: (or 28-162 or 29-162 or 30-162) procorticoliberin #status predicted <MA
F;120-160/Product: corticoliberin 1 #status predicted <CLN>
F;120-159/Domain: diuretic hormone homology <DHH>
F;160/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gly

Query Match 31.3%; Score 56; DB 2; Length 162;
Best Local Similarity 39.4%; Pred. No. 1.1;
Matches 13; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Qy 3 LSLDVPIGLLRILLEQARYKAARNQAATNAQIL 35
:|||: ||| :|| || : || :| :::
Db 125 ISLDLTFHLLREVLEMARAEQLAQQAHSNRKMM 157

RESULT 9
A43978
urotensin I - European flounder
C;Species: Platichthys flesus (European flounder)
C;Date: 11-Feb-1993 #sequence_revision 11-Feb-1993 #text_change 17-May-1996
C;Accession: A43978
R;Conlon, J.M.; Arnold-Reed, D.E.; Balment, R.J.
Peptides 11, 891-895, 1990
A;Title: Urotensin I and its N-terminal flanking peptide from the flounder, Platichthys f
A;Reference number: A43978
A;Accession: A43978
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-41 <CON>
C;Superfamily: corticoliberin-endorpholiberin; diuretic hormone homology
F;1-41/Domain: diuretic hormone homology <DHH>

Query Match 30.2%; Score 54; DB 2; Length 41;
Best Local Similarity 30.6%; Pred. No. 0.44;
Matches 11; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

Qy 3 LSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
:|:|: :|| :: |: : | || | :| |
Db 6 MSIDLTFHMLRNMIHMAKMEGEREQAQINRNLLDEV 41

RESULT 10
S14597
corticoliberin 2 precursor - white sucker
N;Alternate names: corticotropin-releasing factor 2
N;Contains: corticoliberin 2
C;Species: Catostomus commersoni (white sucker)
C;Date: 21-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 22-Oct-1999
C;Accession: S14597
R;Morley, S.D.; Schoenrock, C.; Okawara, Y.; Lederis, K.; Richter, D.
submitted to the EMBL Data Library, March 1991
A;Description: Corticotropin-releasing factor (CRF) gene family in the brain of the tele
one urotensin I peptide.
A;Reference number: S14597
A;Accession: S14597

```
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-162 <MOR>
A;Cross-references: EMBL:X58784; NID:g62599; PIDN:CAA41589.1; PID:g62600
C;Superfamily: corticoliberin-endorpholiberin; diuretic hormone homology
C;Keywords: amidated carboxyl end; hormone
F;1-24/Domain: (or 1-27 or 1-28 or 1-29) signal sequence #status predicted <SIG>
F;25-162/Product: (or 28-162 or 29-162 or 30-162) procorticoliberin #status predicted <M
F;120-160/Product: corticoliberin 2 #status predicted <CLN>
F;120-159/Domain: diuretic hormone homology <DHH>
F;160/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gl

  Query Match             30.2%;  Score 54;  DB 2;  Length 162;
  Best Local Similarity   39.4%;  Pred. No. 2.1;
  Matches   13;  Conservative    8;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQIL 35
              :|||:   ||| :|| || :    || :| :::
Db        125 ISLDLTFHLLREVLEMARAEQLVQQAHSNRKMM 157


RESULT 11
SWFGS
sauvagine - Sauvage's leaf frog
C;Species: Phyllomedusa sauvagei (Sauvage's leaf frog)
C;Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 07-May-1999
C;Accession: A01406; A61325
R;Montecucchi, P.C.; Henschen, A.; Erspamer, V.
Hoppe-Seyler's Z. Physiol. Chem. 360, 1178, 1979
A;Title: Structure of sauvagine, a vasoactive peptide from the skin of a frog.
A;Reference number: A01406
A;Accession: A01406
A;Molecule type: protein
A;Residues: 1-40 <MON>
R;Montecucchi, P.C.; Henschen, A.
Int. J. Pept. Protein Res. 18, 113-120, 1981
A;Title: Amino acid composition and sequence analysis of sauvagine, a new active peptide
A;Reference number: A61325; MUID:82075075; PMID:7309372
A;Accession: A61325
A;Molecule type: protein
A;Residues: 1-40 <MO2>
C;Comment: This hypotensive peptide is obtained from the cutaneous tissue of the frog.
C;Superfamily: corticoliberin-endorpholiberin; diuretic hormone homology
C;Keywords: amidated carboxyl end; antihypertensive; pyroglutamic acid; skin
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;40/Modified site: amidated carboxyl end (Ile) #status experimental

  Query Match             29.6%;  Score 53;  DB 1;  Length 40;
  Best Local Similarity   33.3%;  Pred. No. 0.6;
  Matches   11;  Conservative   10;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQIL 35
              :|:|: : ||| ::|  : :  : ||| | :|
Db          5 ISIDLSLELLRKMIEIEKQEKEKQQAANNRLLL 37


RESULT 12
T04957
hypothetical protein F7J7.200 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
C;Accession: T04957
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X
submitted to the Protein Sequence Database, July 1998
A;Reference number: Z15391
A;Accession: T04957
A;Molecule type: DNA
A;Residues: 1-393 <BEV>
A;Cross-references: EMBL:ALO21960
A;Experimental source: cultivar Columbia; BAC clone F7J7
C;Genetics:
A;Map position: 4
A;Introns: 80/1; 217/3; 264/1; 291/3
A;Note: F7J7.200

  Query Match             29.1%;  Score 52;  DB 2;  Length 393;
  Best Local Similarity   27.3%;  Pred. No. 11;
  Matches    9;  Conservative   13;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQ 33
              ::||| :|: |:  :|  :| :: : |: :| :
Db        231 ILLSLQIPLALVFTILALSRTESLQEQSISNQE 263


RESULT 13
F87709
DNA/pantothenate metabolism flavoprotein [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: F87709
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.F
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolona
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: F87709
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-412 <STO>
A;Cross-references: GB:AE005673; NID:g13425480; PIDN:AAK25674.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC3712
C;Superfamily: pantothenate metabolism flavoprotein dfp

  Query Match             28.5%;  Score 51;  DB 2;  Length 412;
  Best Local Similarity   40.6%;  Pred. No. 16;
  Matches   13;  Conservative    6;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQI 34
              ::|  | |: || :| ||   | :|||  | :
Db        252 VALPTPPGVRRIDVETARQMLAASQAALPADV 283


RESULT 14
T01037
hypothetical protein YUP8H12R.20 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 22-Oct-1999
C;Accession: T01037
R;Theologis, A.; Vysotskaia, V.S.; Osborne, B.I.; Schwartz, J.R.; Federspiel, N.A.; Kwan,
Oefner, P.; Davis, R.W.
submitted to the EMBL Data Library, May 1998
A;Description: Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence.
A;Reference number: Z14227
A;Accession: T01037
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1325 <THE>
A;Cross-references: EMBL:AC002986; NID:g2494106; PID:g3152582; GSPDB:GN00059; ATSP:YUP8H1
C;Genetics:
A;Gene: ATSP:YUP8H12R.20
A;Map position: 1
A;Introns: 70/2; 130/3; 233/3; 384/3; 450/3; 470/1; 687/3; 740/3; 765/3; 868/3; 940/3; 11

  Query Match             28.2%;  Score 50.5;  DB 2;  Length 1325;
  Best Local Similarity   31.2%;  Pred. No. 71;
  Matches   15;  Conservative    5;  Mismatches   11;  Indels   17;  Gaps    1;

Qy          5 LDVPIGLLRILLEQARYKAAR----------------NQAATNAQIL 35
              ||:|:| :| |: : | |                  |||| | ||
Db        481 LDIPLGPVRKLVSEVRVKEYNGEDWQSWCNRTGSGQLVRQAATAACIL 528


RESULT 15
AB1557
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methylated-DNA-protein-cystein methyltransferase homolog lin0995 [imported] - Listeria i
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 11-Jan-2002
C;Accession: AB1557
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1557
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-159 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC96226.1; PID:g16413454; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin0995
C;Superfamily: methylated-DNA-protein-cysteine S-methyltransferase; methylated-DNA-prote
C;Keywords: methylated amino acid
F;125/Binding site: methyl (Cys) (covalent) #status predicted

  Query Match 27.9%; Score 50; DB 2; Length 159;
  Best Local Similarity 38.7%; Pred. No. 7.8;
  Matches 12; Conservative 4; Mismatches 15; Indels 0; Gaps 0;

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Qy          6 DVPIGLLRILLEQARYKAARNQAATNAQILA 36
              | |:| | |::| |          || :|||
Db          7 DSPVGTLFIIIEDAHITKISYDEPTNWEILA 37
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Search completed: April 20, 2004, 18:57:23
Job time : 7.84 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 20, 2004, 18:56:48 ; Search time 57.4933 Seconds
(without alignments)
537.026 Million cell updates/sec

Title: US-09-919-473-10
Perfect score: 557
Sequence: 1 MTRWALVVFVVLMLDRILFV.....KAARNQAATNAQILAHVGRR 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1124875 seqs, 275673149 residues

Total number of hits satisfying chosen parameters: 1124875

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	557	100.0	112	9	US-09-919-473-10	Sequence 10, Appl
2	312	56.0	112	9	US-09-682-706-2	Sequence 2, Appli
3	312	56.0	112	9	US-09-919-473-2	Sequence 2, Appli
4	179	32.1	38	9	US-09-919-473-11	Sequence 11, Appl
5	179	32.1	38	10	US-09-799-978-43	Sequence 43, Appl
6	179	32.1	38	14	US-10-099-766-9	Sequence 9, Appli
7	145	26.0	41	9	US-09-919-473-3	Sequence 3, Appli
8	140	25.1	38	14	US-10-315-964A-114	Sequence 114, App
9	140	25.1	38	14	US-10-317-251A-114	Sequence 114, App
10	140	25.1	38	14	US-10-317-252A-114	Sequence 114, App
11	139	25.0	38	9	US-09-919-473-4	Sequence 4, Appli
12	139	25.0	38	10	US-09-799-978-44	Sequence 44, Appl
13	139	25.0	38	14	US-10-099-766-8	Sequence 8, Appli
14	139	25.0	38	14	US-10-315-964A-4	Sequence 4, Appli
15	139	25.0	38	14	US-10-315-964A-123	Sequence 123, App
16	139	25.0	38	14	US-10-315-964A-354	Sequence 354, App
17	139	25.0	38	14	US-10-317-251A-4	Sequence 4, Appli
18	139	25.0	38	14	US-10-317-251A-123	Sequence 123, App
19	139	25.0	38	14	US-10-317-251A-354	Sequence 354, App
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21	139	25.0	38	14	US-10-317-252A-123	Sequence 123, App
22	139	25.0	38	14	US-10-317-252A-354	Sequence 354, App
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24	139	25.0	39	14	US-10-315-964A-368	Sequence 368, App
25	139	25.0	39	14	US-10-317-251A-356	Sequence 356, App
26	139	25.0	39	14	US-10-317-251A-368	Sequence 368, App
27	139	25.0	39	14	US-10-317-252A-356	Sequence 356, App
28	139	25.0	39	14	US-10-317-252A-368	Sequence 368, App
29	138	24.8	38	14	US-10-315-964A-122	Sequence 122, App
30	138	24.8	38	14	US-10-317-251A-122	Sequence 122, App
31	138	24.8	38	14	US-10-317-252A-122	Sequence 122, App
32	137	24.6	38	14	US-10-315-964A-110	Sequence 110, App
33	137	24.6	38	14	US-10-317-251A-110	Sequence 110, App
34	137	24.6	38	14	US-10-317-252A-110	Sequence 110, App
35	136	24.4	38	14	US-10-315-964A-109	Sequence 109, App
36	136	24.4	38	14	US-10-315-964A-124	Sequence 124, App
37	136	24.4	38	14	US-10-315-964A-127	Sequence 127, App
38	136	24.4	38	14	US-10-315-964A-130	Sequence 130, App
39	136	24.4	38	14	US-10-317-251A-109	Sequence 109, App
40	136	24.4	38	14	US-10-317-251A-124	Sequence 124, App
41	136	24.4	38	14	US-10-317-251A-127	Sequence 127, App
42	136	24.4	38	14	US-10-317-251A-130	Sequence 130, App
43	136	24.4	38	14	US-10-317-252A-109	Sequence 109, App
44	136	24.4	38	14	US-10-317-252A-124	Sequence 124, App
45	136	24.4	38	14	US-10-317-252A-127	Sequence 127, App

ALIGNMENTS

RESULT 1
US-09-919-473-10
; Sequence 10, Application US/09919473
; Patent No. US20020127221A1
; GENERAL INFORMATION:
; APPLICANT: Vale, Wylie Walker Jr.
; APPLICANT: Lewis, Kathy Ann
; APPLICANT: Reyes, Teresa Marie
; APPLICANT: Hogenesch, John Beren
; APPLICANT: Sawchenko, Paul Emil
; APPLICANT: Vaughan, Joan Maureen
; APPLICANT: Rivier, Jean Edouard Frederic
; APPLICANT: Perrin, Marilyn Heller
; TITLE OF INVENTION: Urocortin Proteins and Uses Thereof
; FILE REFERENCE: D6334
; CURRENT APPLICATION NUMBER: US/09/919,473
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/273,969
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 10
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: Mouse Urocortin II precursor peptide
US-09-919-473-10

Query Match 100.0%; Score 557; DB 9; Length 112;
Best Local Similarity 100.0%; Pred. No. 3.4e-52;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MTRWALVVFVVLMLDRILFVPGTPIPTFQLLPQNSLETTPSSVTSESSSGTTTGPSASWS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MTRWALVVFVVLMLDRILFVPGTPIPTFQLLPQNSLETTPSSVTSESSSGTTTGPSASWS 60

Qy         61 NSKASPYLDTRVILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHVGRR 112
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Db         61 NSKASPYLDTRVILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHVGRR 112


RESULT 2
US-09-682-706-2
; Sequence 2, Application US/09682706
; Patent No. US20020082409A1
; GENERAL INFORMATION:
;  APPLICANT: Hsu, Sheau-Yu
;  APPLICANT:  Hsueh, Aaron
;  TITLE OF INVENTION: Stresscopins and their ses
;  FILE REFERENCE: STAN210
;  CURRENT APPLICATION NUMBER: US/09/682,706
;  CURRENT FILING DATE:  2001-10-09
;  PRIOR APPLICATION NUMBER: 60/276,615
;  PRIOR FILING DATE: 2001-03-15
;  PRIOR APPLICATION NUMBER: 60/244,128
;  PRIOR FILING DATE: 2000-10-26
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 112
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-09-682-706-2

  Query Match             56.0%;  Score 312;  DB 9;  Length 112;
  Best Local Similarity   60.9%;  Pred. No. 8.9e-26;
  Matches   67;  Conservative   15;  Mismatches   28;  Indels    0;  Gaps    0;

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              ||| ||:: :|||| |:| || |||||||| |||| :|||    ||| |   | | |: |
Db          1 MTRCALLLLMVLMLGRVLVVPVTPIPTFQLRPQNSPQTTPRPAASESPSAAPTWPWAAQS 60

Qy         61 NSKASPYLDTRVILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHVG 110
              :   : :  :|::|||||||||||:|||||| :||| || |||:||| ||
Db         61 HCSPTRHPGSRIVLSLDVPIGLLQILLEQARARAAREQATTNARILARVG 110


RESULT 3
US-09-919-473-2
; Sequence 2, Application US/09919473
; Patent No. US20020127221A1
; GENERAL INFORMATION:
;  APPLICANT: Vale, Wylie Walker Jr.
;  APPLICANT:  Lewis, Kathy Ann
;  APPLICANT:  Reyes, Teresa Marie
;  APPLICANT:  Hogenesch, John Beren
;  APPLICANT:  Sawchenko, Paul Emil
;  APPLICANT:  Vaughan, Joan Maureen
;  APPLICANT:  Rivier, Jean Edouard Frederic
;  APPLICANT:  Perrin, Marilyn Heller
;  TITLE OF INVENTION: Urocortin Proteins and Uses Thereof
;  FILE REFERENCE: D6334
;  CURRENT APPLICATION NUMBER: US/09/919,473
;  CURRENT FILING DATE:  2001-07-31
;  PRIOR APPLICATION NUMBER: US 60/273,969
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 2
;   LENGTH: 112
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Human Urocortin-related peptide (hURP)
;   OTHER INFORMATION: precursor peptide
US-09-919-473-2

  Query Match             56.0%;  Score 312;  DB 9;  Length 112;
  Best Local Similarity   60.9%;  Pred. No. 8.9e-26;
  Matches   67;  Conservative   15;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          1 MTRWALVVFVVLMLDRILFVPGTPIPTFQLLPQNSLETTPSSVTSESSSGTTTGPSASWS 60
              ||| ||:: :|||| |:| || |||||||| |||| :|||    ||| |   | | |: |
Db          1 MTRCALLLLMVLMLGRVLVVPVTPIPTFQLRPQNSPQTTPRPAASESPSAAPTWPWAAQS 60

Qy         61 NSKASPYLDTRVILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHVG 110
              :   : :  :|::|||||||||||:|||||| :||| || |||:||| ||
Db         61 HCSPTRHPGSRIVLSLDVPIGLLQILLEQARARAAREQATTNARILARVG 110


RESULT 4
US-09-919-473-11
; Sequence 11, Application US/09919473
; Patent No. US20020127221A1
; GENERAL INFORMATION:
;  APPLICANT: Vale, Wylie Walker Jr.
;  APPLICANT:  Lewis, Kathy Ann
;  APPLICANT:  Reyes, Teresa Marie
;  APPLICANT:  Hogenesch, John Beren
;  APPLICANT:  Sawchenko, Paul Emil
;  APPLICANT:  Vaughan, Joan Maureen
;  APPLICANT:  Rivier, Jean Edouard Frederic
;  APPLICANT:  Perrin, Marilyn Heller
;  TITLE OF INVENTION: Urocortin Proteins and Uses Thereof
;  FILE REFERENCE: D6334
;  CURRENT APPLICATION NUMBER: US/09/919,473
;  CURRENT FILING DATE:  2001-07-31
;  PRIOR APPLICATION NUMBER: US 60/273,969
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 11
;   LENGTH: 38
;   TYPE: PRT
;   ORGANISM: Mus musculus
;   FEATURE:
;   OTHER INFORMATION: Mouse Urocortin II
US-09-919-473-11

  Query Match             32.1%;  Score 179;  DB 9;  Length 38;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-12;
  Matches   38;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         72 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 109
              |||||||||||||||||||||||||||||||||||||
Db          1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38


RESULT 5
US-09-799-978-43
; Sequence 43, Application US/09799978
; Publication No. US20030165807A1
; GENERAL INFORMATION:
;  APPLICANT:  The Procter & Gamble Company
;  APPLICANT:  Isfort, Robert
;  APPLICANT:  Sheldon, Russell
;  TITLE OF INVENTION:   Methods for Identifying Compounds for Regulating Muscle Mass or
;  TITLE OF INVENTION:  Function Using Corticotropin Releasing Factor Receptors
;  FILE REFERENCE:   8448
;  CURRENT APPLICATION NUMBER: US/09/799,978
;  CURRENT FILING DATE:  2001-03-06
;  NUMBER OF SEQ ID NOS:   44
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 43
;   LENGTH: 38
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-799-978-43

  Query Match             32.1%;  Score 179;  DB 10;  Length 38;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-12;
  Matches   38;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         72 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 109
              |||||||||||||||||||||||||||||||||||||
Db          1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
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RESULT 6
US-10-099-766-9
; Sequence 9, Application US/10099766
; Publication No. US20030036507A1
; GENERAL INFORMATION:
; APPLICANT: Lewis, Kathy
; APPLICANT: Vale, Wylie
; APPLICANT: Marilyn H. Perrin
; APPLICANT: Jean E. Rivier
; APPLICANT: Koichi S. Kunitake
; APPLICANT: Joszef Gulyas
; TITLE OF INVENTION: Urocortin III and Uses Thereof
; FILE REFERENCE: D6390
; CURRENT APPLICATION NUMBER: US/10/099,766
; CURRENT FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/276,069
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 9
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: Mouse Urocortin II (mUcn II)
US-10-099-766-9

Query Match 32.1%; Score 179; DB 14; Length 38;
Best Local Similarity 100.0%; Pred. No. 4.8e-12;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 109
||||||||||||||||||||||||||||||||||||||
Db 1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38

RESULT 7
US-09-919-473-3
; Sequence 3, Application US/09919473
; Patent No. US20020127221A1
; GENERAL INFORMATION:
; APPLICANT: Vale, Wylie Walker Jr.
; APPLICANT: Lewis, Kathy Ann
; APPLICANT: Reyes, Teresa Marie
; APPLICANT: Hogenesch, John Beren
; APPLICANT: Sawchenko, Paul Emil
; APPLICANT: Vaughan, Joan Maureen
; APPLICANT: Rivier, Jean Edouard Frederic
; APPLICANT: Perrin, Marilyn Heller
; TITLE OF INVENTION: Urocortin Proteins and Uses Thereof
; FILE REFERENCE: D6334
; CURRENT APPLICATION NUMBER: US/09/919,473
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/273,969
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 3
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human Urocortin-related peptide (hURP)
US-09-919-473-3

Query Match 26.0%; Score 145; DB 9; Length 41;
Best Local Similarity 76.9%; Pred. No. 2.4e-08;
Matches 30; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 72 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHVG 110
::|||||||||:|||||| :||| || |||:||| ||
Db 1 IVLSLDVPIGLLQILLEQARARAAREQATTNARILARVG 39

RESULT 8
US-10-315-964A-114
; Sequence 114, Application US/10315964A
; Publication No. US20030148956A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert J
; APPLICANT: Mazur, Wieslaw A
; TITLE OF INVENTION: Cortcotropin Releasing Factor 2 Receptor Agonists
; FILE REFERENCE: 8847M3
; CURRENT APPLICATION NUMBER: US/10/315,964A
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: US 60/349,117
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: US 60/376,337
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/388,895
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/411,988
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 530
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 114
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized artificial peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (38)..(38)
; OTHER INFORMATION: AMIDATION
US-10-315-964A-114

Query Match 25.1%; Score 140; DB 14; Length 38;
Best Local Similarity 76.3%; Pred. No. 7.7e-08;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 72 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 109
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Db 1 IVLSLDVPIGLLQILLEQARQRAAREQATTNARILARV 38

RESULT 9
US-10-317-251A-114
; Sequence 114, Application US/10317251A
; Publication No. US20030148957A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert J
; APPLICANT: Mazur, Wieslaw A
; TITLE OF INVENTION: Cortcotropin Releasing Factor 2 Receptor Agonists
; FILE REFERENCE: 8847M2
; CURRENT APPLICATION NUMBER: US/10/317,251A
; CURRENT FILING DATE: 2002-12-11
; PRIOR APPLICATION NUMBER: US 60/349,117
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: US 60/376,337
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/388,895
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/411,988
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 530
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 114
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized artificial peptide
; FEATURE:

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;   NAME/KEY: MOD_RES
;   LOCATION: (38)..(38)
;   OTHER INFORMATION: AMIDATION
US-10-317-251A-114

  Query Match             25.1%;  Score 140;  DB 14;  Length 38;
  Best Local Similarity   76.3%;  Pred. No. 7.7e-08;
  Matches   29;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         72 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 109
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Db          1 IVLSLDVPIGLLQILLEQARQRAAREQATTNARILARV 38


RESULT 10
US-10-317-252A-114
; Sequence 114, Application US/10317252A
; Publication No. US20030148958A1
; GENERAL INFORMATION:
;  APPLICANT: The Procter & Gamble Company
;  APPLICANT:  Isfort, Robert J
;  APPLICANT:  Mazur, Wieslaw A
;  TITLE OF INVENTION: Cortcotropin Releasing Factor 2 Receptor Agonists
;  FILE REFERENCE: 8847M
;  CURRENT APPLICATION NUMBER: US/10/317,252A
;  CURRENT FILING DATE:  2003-03-31
;  PRIOR APPLICATION NUMBER: US 60/349,117
;  PRIOR FILING DATE: 2002-01-16
;  PRIOR APPLICATION NUMBER: US 60/376,337
;  PRIOR FILING DATE: 2002-04-29
;  PRIOR APPLICATION NUMBER: US 60/388,895
;  PRIOR FILING DATE: 2002-06-14
;  PRIOR APPLICATION NUMBER: US 60/411,988
;  PRIOR FILING DATE: 2002-09-19
;  NUMBER OF SEQ ID NOS: 530
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 114
;   LENGTH: 38
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Chemically synthesized artificial peptide
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (38)..(38)
;   OTHER INFORMATION: AMIDATION
US-10-317-252A-114

  Query Match             25.1%;  Score 140;  DB 14;  Length 38;
  Best Local Similarity   76.3%;  Pred. No. 7.7e-08;
  Matches   29;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         72 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 109
              ::|||||||||||:|||||| :||| || |||:||| |
Db          1 IVLSLDVPIGLLQILLEQARQRAAREQATTNARILARV 38


RESULT 11
US-09-919-473-4
; Sequence 4, Application US/09919473
; Patent No. US20020127221A1
; GENERAL INFORMATION:
;  APPLICANT: Vale, Wylie Walker Jr.
;  APPLICANT:  Lewis, Kathy Ann
;  APPLICANT:  Reyes, Teresa Marie
;  APPLICANT:  Hogenesch, John Beren
;  APPLICANT:  Sawchenko, Paul Emil
;  APPLICANT:  Vaughan, Joan Maureen
;  APPLICANT:  Rivier, Jean Edouard Frederic
;  APPLICANT:  Perrin, Marilyn Heller
;  TITLE OF INVENTION: Urocortin Proteins and Uses Thereof
;  FILE REFERENCE: D6334
;  CURRENT APPLICATION NUMBER: US/09/919,473
;  CURRENT FILING DATE:  2001-07-31
;  PRIOR APPLICATION NUMBER: US 60/273,969
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 4
;   LENGTH: 38
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Amino acids 1-38 of human
;   OTHER INFORMATION: Urocortin-related peptide (hURP)
US-09-919-473-4

  Query Match             25.0%;  Score 139;  DB 9;  Length 38;
  Best Local Similarity   76.3%;  Pred. No. 9.8e-08;
  Matches   29;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         72 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 109
              ::|||||||||||:|||||| :||| || |||:||| |
Db          1 IVLSLDVPIGLLQILLEQARARAAREQATTNARILARV 38


RESULT 12
US-09-799-978-44
; Sequence 44, Application US/09799978
; Publication No. US20030165807A1
; GENERAL INFORMATION:
;  APPLICANT:  The Procter & Gamble Company
;  APPLICANT:  Isfort, Robert
;  APPLICANT:  Sheldon, Russell
;  TITLE OF INVENTION:   Methods for Identifying Compounds for Regulating Muscle Mass or
;  TITLE OF INVENTION:  Function Using Corticotropin Releasing Factor Receptors
;  FILE REFERENCE:   8448
;  CURRENT APPLICATION NUMBER: US/09/799,978
;  CURRENT FILING DATE:  2001-03-06
;  NUMBER OF SEQ ID NOS:   44
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 44
;   LENGTH: 38
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-799-978-44

  Query Match             25.0%;  Score 139;  DB 10;  Length 38;
  Best Local Similarity   76.3%;  Pred. No. 9.8e-08;
  Matches   29;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         72 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 109
              ::|||||||||||:|||||| :||| || |||:||| |
Db          1 IVLSLDVPIGLLQILLEQARARAAREQATTNARILARV 38


RESULT 13
US-10-099-766-8
; Sequence 8, Application US/10099766
; Publication No. US20030036507A1
; GENERAL INFORMATION:
;  APPLICANT: Lewis, Kathy
;  APPLICANT:  Vale, Wylie
;  APPLICANT:  Marilyn H. Perrin
;  APPLICANT:  Jean E. Rivier
;  APPLICANT:  Koichi S. Kunitake
;  APPLICANT:  Joszef Gulyas
;  TITLE OF INVENTION: Urocortin III and Uses Thereof
;  FILE REFERENCE: D6390
;  CURRENT APPLICATION NUMBER: US/10/099,766
;  CURRENT FILING DATE:  2002-03-15
;  PRIOR APPLICATION NUMBER: US 60/276,069
;  PRIOR FILING DATE: 2001-03-15
;  NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 8
;   LENGTH: 38
;   TYPE: PRT
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;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Human Urocortin-related peptide (hURP),
;   OTHER INFORMATION: human urocortin II
US-10-099-766-8

  Query Match             25.0%;  Score 139;  DB 14;  Length 38;
  Best Local Similarity   76.3%;  Pred. No. 9.8e-08;
  Matches   29;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         72 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 109
              ::||||||||||:|||||| :||| || |||:||| |
Db          1 IVLSLDVPIGLLQILLEQARARAAREQATTNARILARV 38


RESULT 14
US-10-315-964A-4
; Sequence 4, Application US/10315964A
; Publication No. US20030148956A1
; GENERAL INFORMATION:
;  APPLICANT: The Procter & Gamble Company
;  APPLICANT:  Isfort, Robert J
;  APPLICANT:  Mazur, Wieslaw A
;  TITLE OF INVENTION: Cortcotropin Releasing Factor 2 Receptor Agonists
;  FILE REFERENCE: 8847M3
;  CURRENT APPLICATION NUMBER: US/10/315,964A
;  CURRENT FILING DATE:  2003-04-01
;  PRIOR APPLICATION NUMBER: US 60/349,117
;  PRIOR FILING DATE: 2002-01-16
;  PRIOR APPLICATION NUMBER: US 60/376,337
;  PRIOR FILING DATE: 2002-04-29
;  PRIOR APPLICATION NUMBER: US 60/388,895
;  PRIOR FILING DATE: 2002-06-14
;  PRIOR APPLICATION NUMBER: US 60/411,988
;  PRIOR FILING DATE: 2002-09-19
;  NUMBER OF SEQ ID NOS: 530
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 38
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-315-964A-4

  Query Match             25.0%;  Score 139;  DB 14;  Length 38;
  Best Local Similarity   76.3%;  Pred. No. 9.8e-08;
  Matches   29;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         72 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 109
              ::||||||||||:|||||| :||| || |||:||| |
Db          1 IVLSLDVPIGLLQILLEQARARAAREQATTNARILARV 38


RESULT 15
US-10-315-964A-123
; Sequence 123, Application US/10315964A
; Publication No. US20030148956A1
; GENERAL INFORMATION:
;  APPLICANT: The Procter & Gamble Company
;  APPLICANT:  Isfort, Robert J
;  APPLICANT:  Mazur, Wieslaw A
;  TITLE OF INVENTION: Cortcotropin Releasing Factor 2 Receptor Agonists
;  FILE REFERENCE: 8847M3
;  CURRENT APPLICATION NUMBER: US/10/315,964A
;  CURRENT FILING DATE:  2003-04-01
;  PRIOR APPLICATION NUMBER: US 60/349,117
;  PRIOR FILING DATE: 2002-01-16
;  PRIOR APPLICATION NUMBER: US 60/376,337
;  PRIOR FILING DATE: 2002-04-29
;  PRIOR APPLICATION NUMBER: US 60/388,895
;  PRIOR FILING DATE: 2002-06-14
;  PRIOR APPLICATION NUMBER: US 60/411,988
;  PRIOR FILING DATE: 2002-09-19
;  NUMBER OF SEQ ID NOS: 530
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 123
;   LENGTH: 38
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Chemically synthesized artificial peptide
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (38)..(38)
;   OTHER INFORMATION: AMIDATION
US-10-315-964A-123

  Query Match             25.0%;  Score 139;  DB 14;  Length 38;
  Best Local Similarity   76.3%;  Pred. No. 9.8e-08;
  Matches   29;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         72 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 109
              ::||||||||||:|||||| :||| || |||:||| |
Db          1 IVLSLDVPIGLLQILLEQARQEAAREQATTNARILARV 38


Search completed: April 20, 2004, 19:06:53
Job time : 89.4933 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 20, 2004, 18:51:47 ; Search time 53.76 Seconds
(without alignments)
657.330 Million cell updates/sec

Title: US-09-919-473-10
Perfect score: 557
Sequence: 1 MTRWALVVFVVLMLDRILFV.....KAARNQAATNAQILAHVGRR 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	117	21.0	151	13	Q9I8E5	Q9i8e5 fugu rubrip
2	89.5	16.1	157	5	Q9W1K2	Q9w1k2 drosophila
3	84.5	15.2	499	5	Q9VJE1	Q9vje1 drosophila
4	81	14.5	119	5	Q9VPT0	Q9vpt0 drosophila
5	80.5	14.5	649	11	Q8BKD5	Q8bkd5 mus musculu
6	80.5	14.5	1450	11	Q80T94	Q80t94 mus musculu
7	79.5	14.3	187	11	Q8CIT0	Q8cit0 mus musculu
8	79	14.2	338	3	O42882	O42882 schizosacch
9	78.5	14.1	603	4	Q9H6V7	Q9h6v7 homo sapien
10	78.5	14.1	920	4	Q9H3X4	Q9h3x4 homo sapien
11	78.5	14.1	924	4	Q9NVI9	Q9nvi9 homo sapien
12	78.5	14.1	924	4	Q9H7S3	Q9h7s3 homo sapien
13	78.5	14.1	924	4	Q8WUB6	Q8wub6 homo sapien
14	78.5	14.1	1409	4	Q9C0A6	Q9c0a6 homo sapien
15	77.5	13.9	889	2	Q9X6X6	Q9x6x6 salmonella
16	77.5	13.9	889	16	Q8ZNH2	Q8znh2 salmonella
17	77.5	13.9	889	16	Q8Z563	Q8z563 salmonella
18	77.5	13.9	889	16	Q83T68	Q83t68 salmonella
19	76.5	13.7	592	16	Q8NRG2	Q8nrg2 corynebacte
20	76.5	13.7	699	11	Q9Z0Y5	Q9z0y5 mus musculu
21	76.5	13.7	751	11	Q9R218	Q9r218 mus musculu
22	76	13.6	542	3	Q9URQ4	Q9urq4 saccharomyc
23	76	13.6	579	5	Q8I1C6	Q8i1c6 drosophila
24	75.5	13.6	1337	1	Q9Y8I8	Q9y8i8 thermococcu
25	75.5	13.6	2093	4	Q15010	Q15010 homo sapien
26	75.5	13.6	2119	4	Q86XD3	Q86xd3 homo sapien
27	75	13.5	195	5	Q9BIH2	Q9bih2 anopheles g
28	75	13.5	346	8	Q8SHH8	Q8shh8 chamaeleo e
29	75	13.5	1286	2	Q84IQ2	Q84iq2 bacillus gl
30	74.5	13.4	756	5	O44418	O44418 chironomus
31	74.5	13.4	756	5	O44417	O44417 chironomus
32	73.5	13.2	164	4	Q14851	Q14851 homo sapien
33	73.5	13.2	506	5	Q86KV8	Q86kv8 dictyosteli
34	73.5	13.2	712	4	Q8N5C8	Q8n5c8 homo sapien
35	73.5	13.2	2344	5	Q86H67	Q86h67 dictyosteli
36	73.5	13.2	22152	4	Q8WXI7	Q8wxi7 homo sapien
37	73	13.1	125	17	Q9Y940	Q9y940 aeropyrum p
38	73	13.1	528	3	Q874N8	Q874n8 candida gla
39	73	13.1	802	16	Q9A511	Q9a511 caulobacter
40	72.5	13.0	232	16	Q83JR1	Q83jr1 shigella fl
41	72.5	13.0	526	2	O85316	O85316 salmonella
42	72.5	13.0	803	5	Q86J08	Q86j08 dictyosteli
43	72.5	13.0	1496	4	Q92626	Q92626 homo sapien
44	72.5	13.0	1983	5	Q9U165	Q9u165 leishmania
45	72.5	13.0	3283	16	Q8Z1S2	Q8z1s2 salmonella

ALIGNMENTS

RESULT 1
Q9I8E5
ID Q9I8E5 PRELIMINARY; PRT; 151 AA.
AC Q9I8E5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Urocortin precursor.
GN UCN.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetradontoidea; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20485066; PubMed=11032317;
RA Brunner B., Gruetzner F., Yaspo M.L., Ropers H.H., Haaf T.,
RA Kalscheuer V.M.;
RT "Molecular cloning and characterization of the Fugu rubripes
RT MEST/COPG2 imprinting cluster and chromosomal localization in Fugu and
RT Tetraodon nigroviridis.";
RL Chromosome Res. 8:465-476(2000).
DR EMBL; AJ251323; CAB96535.1; -.
KW Signal.
FT SIGNAL 1 20 POTENTIAL.
SQ SEQUENCE 151 AA; 16686 MW; EEB1D52C41A67124 CRC64;

Query Match 21.0%; Score 117; DB 13; Length 151;
Best Local Similarity 33.3%; Pred. No. 8.9e-05;
Matches 36; Conservative 21; Mismatches 31; Indels 20; Gaps 4;

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Qy          20 VPG-TPIPTFQLLPQNSLETTPSSVTSESSSGTTTGPSASW----------SNSKA 64
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Db          48 VPGYSPADDWASLLQSAY---LSSSSAESSREKRTAAPANYRFLRRTKLRGQMLRNSSKG 104

Qy          65 SPYLDTRVILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHVGRR 112
                  ·|· ||||||  ·· ·| · |· |  | ·|| ||::|||·|||
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Db        105 D--RRSRLTLSLDVPTNIMNVLFDVAKAKNLRAKAAENARLLAHIGRR 150


RESULT 2
Q9W1K2
ID   Q9W1K2      PRELIMINARY;      PRT;   157 AA.
AC   Q9W1K2;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   CG12491 protein.
GN   CG12491.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
DR   EMBL; AE003461; AAF47056.1; -.
DR   FlyBase; FBgn0034900; CG12491.
SQ   SEQUENCE   157 AA;  16832 MW;  DD27EEB4827E7914 CRC64;

  Query Match             16.1%;  Score 89.5;  DB 5;  Length 157;
  Best Local Similarity   33.3%;  Pred. No. 0.092;
  Matches   27;  Conservative   13;  Mismatches   40;  Indels    1;  Gaps    1;

Qy         32 PQNSLETTPSSVTSESSSGTTTGPSASWSNSKASPYLDTRVILSLDVPIGLLRILLEQAR 91
              | :|  |:|:| || |:: ||| || |   | :|   |:  :  |   :  || |  | |
Db         73 PSSSSSTSPTSSTS-STTATTTAPSTSSDTSSSSTSSDSEEVDRLRRRLRRLRRLRRQER 131

Qy         92 YKAARNQAATNAQILAHVGRR 112
                 :  | :    :  :  |||


Db        132 RQEIRRERQQERRQQSRAGRR 152


RESULT 3
Q9VJE1
ID   Q9VJE1      PRELIMINARY;      PRT;   499 AA.
AC   Q9VJE1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   CG5043 protein.
GN   CG5043.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
DR   EMBL; AE003655; AAF53609.1; -.
DR   FlyBase; FBgn0032636; CG5043.
SQ   SEQUENCE   499 AA;  57015 MW;  564A43D68F447FD3 CRC64;

  Query Match             15.2%;  Score 84.5;  DB 5;  Length 499;
  Best Local Similarity   30.2%;  Pred. No. 1.4;
  Matches   29;  Conservative   17;  Mismatches   29;  Indels   21;  Gaps    4;

Qy         29 QLLPQNSLETTPSSVTSESSSGTTTGPSASWSNSKAS---------PYL-----DTRVIL 74
              | :|:  |  |  ||  | :::|:::| |:  : :| |           |||       |  ::
Db         64 QKIPETGLLTPSSSDNSLTTTGSSSGQSSCSAMAKTSLLREPTSLTPYLTLKRQQTSTLI 123

Qy         75 SLDVPIGLLRILLEQARYKAARNQAATNAQILAHVG 110
              :  |      |  | |  :| ||      | |::||||


Db        132 RQEIRRERQQERRQQSRAGRR 152
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Db        124 NFRV-----RKSLSQMDFKEARRTG--NYQLVAHVG 152


RESULT 4
Q9VPT0
ID   Q9VPT0      PRELIMINARY;      PRT;   119 AA.
AC   Q9VPT0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   CG13947 protein.
GN   CG13947.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
DR   EMBL; AE003588; AAF51462.1; -.
DR   FlyBase; FBgn0031277; CG13947.
SQ   SEQUENCE   119 AA;  10924 MW;  7036DA38658CA43C CRC64;

  Query Match             14.5%;  Score 81;  DB 5;  Length 119;
  Best Local Similarity   47.8%;  Pred. No. 0.54;
  Matches   22;  Conservative    5;  Mismatches   15;  Indels    4;  Gaps    2;

Qy         21 PGTP--IPTFQLLPQNSLETTPSSVTSESSSGTTTGPSASWSNSKA 64
              || |  :|    || ||  || :| |:|||: |||   ||  :| |
Db         76 PGGPWGLPPNATLPSNSTTTTTTSTTTESSTSTTT--EASTESSPA 119


RESULT 5
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```
Q8BKD5
ID   Q8BKD5      PRELIMINARY;      PRT;   649 AA.
AC   Q8BKD5;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   PLACE4000063 protein homolog.
GN   2900045N06RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Eye;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK053541; BAC35420.1; -.
DR   MGD; MGI:1920145; 2900045N06Rik.
SQ   SEQUENCE   649 AA;  68981 MW;  CEFA3C76B4496610 CRC64;

  Query Match             14.5%;  Score 80.5;  DB 11;  Length 649;
  Best Local Similarity   28.3%;  Pred. No. 5.3;
  Matches   34;  Conservative   12;  Mismatches   41;  Indels   33;  Gaps    5;

Qy         21 PGTPIPTFQLLPQNSLETTPSSVTSESSSGTTTG---PSASWSNSKASP---------- 66
              |  |: |  | |       ||   :|:  || :||    |  | |:| |||
Db        509 PAHPVSTDSLAP---FTGTPGYYSSQPHSGNSTGSNLPRRSCSSSAASPTPQGPSDSPTS 565

Qy         67 ----YLDTRVILSL--------DVPIGLLRILL----EQARYKAARNQAATNAQILAHVG 110
                  |  : |           :| |  | | |    : | |:|:|  | :|:|   | |
Db        566 DSVSQSSTGTLSSTSFPQNSRSSLPSDLRTISLPNAGQSAAYQASRVSAVSNSQHYPHRG 625


RESULT 6
Q80T94
ID   Q80T94      PRELIMINARY;      PRT;  1450 AA.
AC   Q80T94;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   MKIAA1757 protein (Fragment).
GN   MKIAA1757.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22579291; PubMed=12693553;
RA   Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,
RA   Nakajima D., Nagase T., Ohara O., Koga H.;
RT   "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT   II. The complete nucleotide sequences of 400 mouse KIAA-homologous
RT   cDNAs identified by screening of terminal sequences of cDNA clones
RT   randomly sampled from size-fractionated libraries.";
RL   DNA Res. 10:35-48(2003).
DR   EMBL; AK122551; BAC65833.1; -.
DR   InterPro; IPR001214; SET.
DR   Pfam; PF00856; SET; 1.
DR   SMART; SM00317; SET; 1.
DR   PROSITE; PS50280; SET; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   1450 AA;  158350 MW;  320136D1BC64C45B CRC64;

  Query Match             14.5%;  Score 80.5;  DB 11;  Length 1450;
  Best Local Similarity   28.3%;  Pred. No. 15;
  Matches   34;  Conservative   12;  Mismatches   41;  Indels   33;  Gaps    5;
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Qy          21 PGTPIPTFQLLPQNSLETTPSSVTSESSSGTTTG---PSASWSNSKASP---------- 66
               |  |: |  | |       ||   :|:  || :||   |  | |:| |||
Db        1310 PAHPVSTDSLAP---FTGTPGYYSSQPHSGNSTGSNLPRRSCSSSAASPTPQGPSDSPTS 1366

Qy          67 ----YLDTRVILSL--------DVPIGLLRILL----EQARYKAARNQAATNAQILAHVG 110
                    |  : |          :|  |  | |    :  | |:|:|  | :|:|   | |
Db        1367 DSVSQSSTGTLSSTSFPQNSRSSLPSDLRTISLPNAGQSAAYQASRVSAVSNSQHYPHRG 1426


RESULT 7
Q8CIT0
ID   Q8CIT0      PRELIMINARY;      PRT;   187 AA.
AC   Q8CIT0;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Preprocorticotropin-releasing hormone.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RA   Seasholtz A.F., Bourbonais F.J., Harnden C.E., Camper S.A.;
RT   "Nucleotide Sequence and Expression of the Mouse Corticotropin-
RT   Releasing Hormone Gene.";
RL   Mol. Cell. Neurosci. 2:266-273(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RA   Seasholtz A.F., Bourbonais F.J., Harnden C.E., Camper S.A.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY128673; AAN07905.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR000187; corticoliberin.
DR   InterPro; IPR003620; Urocortin_CRF.
DR   Pfam; PF00473; CRF; 1.
DR   PRINTS; PR01612; CRFFAMILY.
DR   ProDom; PD005970; Urocortin_CRF; 1.
DR   SMART; SM00039; CRF; 1.
DR   PROSITE; PS00511; CRF; 1.
FT   CHAIN       145    187       CORTICOTROPIN-RELEASING HORMONE.
SQ   SEQUENCE   187 AA;  20778 MW;  5E51665291FAA998 CRC64;

  Query Match             14.3%;  Score 79.5;  DB 11;  Length 187;
  Best Local Similarity   28.9%;  Pred. No. 1.4;
  Matches   24;  Conservative   17;  Mismatches   33;  Indels    9;  Gaps    2;

Qy          31 LPQNSLET--TPSSVTSESSSGTTTGPSASWSNSKASPYLDTRVILSLDVPIGLLRILLE 88
               :|| ||::   |:   :| : |   |        |:  |       :|||:   ||| :||
Db        112 MPQRSLDSRAEPAERGAEDALGGHQGALERERRSEEPP-------ISLDLTFHLLREVLE 164

Qy          89 QARYKAARNQAATNAQILAHVGR 111
                  || :    || :| ::: :|:
Db        165 MARAEQLAQQAHSNRKLMEIIGK 187


RESULT 8
O42882
ID   O42882      PRELIMINARY;      PRT;   338 AA.
AC   O42882;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical protein.
GN   SPAC8E11.05C.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972h-;
RA   McLean J., Harris D., Wood V., Barrell B.G., Rajandream M.A.;
RL   Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL021817; CAA17026.1; -.
DR   PIR; T39159; T39159.
DR   GeneDB_SPombe; SPAC8E11.05c; -.
KW   Hypothetical protein.
SQ   SEQUENCE   338 AA;  38200 MW;  252D3319E127C6BF CRC64;

  Query Match             14.2%;  Score 79;  DB 3;  Length 338;
  Best Local Similarity   27.7%;  Pred. No. 3.4;
  Matches   28;  Conservative    9;  Mismatches   28;  Indels   36;  Gaps    3;

Qy           8 VFVVLMLDRILFVPGTPIPTFQLLPQNSLETTPSSVTSESSSGTTTGPSASWSNSKASPY 67
               :|:| |        | |:   :|||      |||:  | :|| |    | :   |:  ||
Db         202 IFLVTM--------GLPVDLDELLP------TPSTQGSFNSSRTIELSSVTLPKSEDEPY 247

Qy          68 LDTRVILSLDVPIGLLRILLEQARYKAARNQAATNAQILAH 108
               ||                    | |||   : |   | |
Db         248 LD----------------------YSAARRLCSINKDALTH 266


RESULT 9
Q9H6V7
ID   Q9H6V7      PRELIMINARY;      PRT;   603 AA.
AC   Q9H6V7;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Hypothetical protein FLJ21825.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA   Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
RA   Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK025478; BAB15144.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   603 AA;  63563 MW;  1CA4AEBCA9F83D50 CRC64;

  Query Match             14.1%;  Score 78.5;  DB 4;  Length 603;
  Best Local Similarity   28.3%;  Pred. No. 8;
  Matches   34;  Conservative   12;  Mismatches   41;  Indels   33;  Gaps    5;

Qy          21 PGTPIPTFQLLPQNSLETTPSSVTSESSSGTTTG---PSASWSNSKASPYL--------- 68
               |  |: |  | |       ||   :|:  || :||   |  |  :| ||| |
Db        463 PAHPVSTDSLAP---FTGTPGYFSSQPHSGNSTGSNLPRRSCPSSAASPTLQGPSDSPTS 519

Qy          69 ------DTRVILSL--------DVPIGLLRILL----EQARYKAARNQAATNAQILAHVG 110
                     |  : |          :|  |  | |    :  | |:|:|  | :|:|   | |
Db        520 DSVSQSSTGTLSSTSFPQNSRSSLPSDLRTISLPSAGQSAVYQASRVSAVSNSQHYPHRG 579


RESULT 10
Q9H3X4
ID   Q9H3X4      PRELIMINARY;      PRT;   920 AA.
AC   Q9H3X4;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Hypothetical protein (Fragment).
GN   DKFZP761P157.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Amygdala;
RA   Koehrer K., Beyer A., Mewes H.W., Weil B., Wiemann S.;
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL442073; CAC09439.1; -.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   920 AA;  98580 MW;  5E65FF2686511DAC CRC64;

  Query Match             14.1%;  Score 78.5;  DB 4;  Length 920;
  Best Local Similarity   28.3%;  Pred. No. 14;
  Matches   34;  Conservative   12;  Mismatches   41;  Indels   33;  Gaps    5;

Qy         21 PGTPIPTFQLLPQNSLETTPSSVTSESSSGTTTG---PSASWSNSKASPYL--------- 68
              |  |: |  | |      ||   :|:  || :||   |  |  :| ||| |
Db        780 PAHPVSTDSLAP---FTGTPGYFSSQPHSGNSTGSNLPRRSCPSSAASPTLQGPSDSPTS 836

Qy         69 ------DTRVILSL--------DVPIGLLRILL----EQARYKAARNQAATNAQILAHVG 110
                   |  : |          :|  |  | |    : | |:|:|  | :|:|   | |
Db        837 DSVSQSSTGTLSSTSFPQNSRSSLPSDLRTISLPSAGQSAVYQASRVSAVSNSQHYPHRG 896


RESULT 11
Q9NVI9
ID   Q9NVI9      PRELIMINARY;      PRT;   924 AA.
AC   Q9NVI9;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Hypothetical protein FLJ10707.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA   Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA   Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA   Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA   Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA   Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA   Ninomiya K., Iwayanagi T.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK001569; BAA91762.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   924 AA;  99092 MW;  9EAC1C3D92A44CEE CRC64;

  Query Match             14.1%;  Score 78.5;  DB 4;  Length 924;
  Best Local Similarity   28.3%;  Pred. No. 14;
  Matches   34;  Conservative   12;  Mismatches   41;  Indels   33;  Gaps    5;

Qy         21 PGTPIPTFQLLPQNSLETTPSSVTSESSSGTTTG---PSASWSNSKASPYL--------- 68
              |  |: |  | |      ||   :|:  || :||   |  |  :| ||| |
Db        784 PAHPVSTDSLAP---FTGTPGYFSSQPHSGNSTGSNLPRRSCPSSAASPTLQGPSDSPTS 840

Qy         69 ------DTRVILSL--------DVPIGLLRILL----EQARYKAARNQAATNAQILAHVG 110
                   |  : |          :|  |  | |    : | |:|:|  | :|:|   | |
Db        841 DSVSQSSTGTLSSTSFPQNSRSSLPSDLRTISLPSAGQSAVYQASRVSAVSNSQHYPHRG 900


RESULT 12
Q9H7S3
ID   Q9H7S3      PRELIMINARY;      PRT;   924 AA.
AC   Q9H7S3;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Hypothetical protein FLJ14322.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RA   Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA   Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA   Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
RA   Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA   Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK024384; BAB14903.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   924 AA;  99072 MW;  358150B216B8C881 CRC64;

  Query Match             14.1%;  Score 78.5;  DB 4;  Length 924;
  Best Local Similarity   28.3%;  Pred. No. 14;
  Matches   34;  Conservative   12;  Mismatches   41;  Indels   33;  Gaps    5;

Qy         21 PGTPIPTFQLLPQNSLETTPSSVTSESSSGTTTG---PSASWSNSKASPYL--------- 68
              |  |: |  | |      ||   :|:  || :||   |  |  :| ||| |
Db        784 PAHPVSTDSLAP---FTGTPGYFSSQPHSGNSTGSNLPRRSCPSSAASPTLQGPSDSPTS 840

Qy         69 ------DTRVILSL--------DVPIGLLRILL----EQARYKAARNQAATNAQILAHVG 110
                   |  : |          :|  |  | |    : | |:|:|  | :|:|   | |
Db        841 DSVSQSSTGTLSSTSFPQNSRSSLPSDLRTISLPSAGQSAVYQASRVSAVSNSQHYPHRG 900


RESULT 13
Q8WUB6
ID   Q8WUB6      PRELIMINARY;      PRT;   924 AA.
AC   Q8WUB6;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Colon;
RA   Strausberg R.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC020956; AAH20956.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   924 AA;  99082 MW;  9A3CC00E2537C99F CRC64;

  Query Match             14.1%;  Score 78.5;  DB 4;  Length 924;
  Best Local Similarity   28.3%;  Pred. No. 14;
  Matches   34;  Conservative   12;  Mismatches   41;  Indels   33;  Gaps    5;

Qy         21 PGTPIPTFQLLPQNSLETTPSSVTSESSSGTTTG---PSASWSNSKASPYL--------- 68
              |  |: |  | |      ||   :|:  || :||   |  |  :| ||| |
Db        784 PAHPVSTDSLAP---FTGTPGYFSSQPHSGNSTGSNLPRRSCPSSAASPTLQGPSDSPTS 840

Qy         69 ------DTRVILSL--------DVPIGLLRILL----EQARYKAARNQAATNAQILAHVG 110
                   |  : |          :|  |  | |    : | |:|:|  | :|:|   | |
Db        841 DSVSQSSTGTLSSTSFPQNSRSSLPSDLRTISLPSAGQSAVYQASRVSAVSNSQHYPHRG 900


RESULT 14
Q9C0A6
ID   Q9C0A6      PRELIMINARY;      PRT;  1409 AA.
AC   Q9C0A6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein KIAA1757 (Fragment).
GN   KIAA1757.
```

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OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21082932; PubMed=11214970;
RA   Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes. XIX.
RT   The complete sequences of 100 new cDNA clones from brain which code
RT   for large proteins in vitro.";
RL   DNA Res. 7:347-355(2000).
CC   -!- SIMILARITY: CONTAINS 1 SET DOMAIN.
DR   EMBL; AB051544; BAB21848.1; -.
DR   InterPro; IPR001214; SET.
DR   Pfam; PF00856; SET; 1.
DR   SMART; SM00317; SET; 1.
DR   PROSITE; PS50280; SET; 1.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   1409 AA;  154203 MW;  B8ED7A94B6AC0606 CRC64;

  Query Match             14.1%;  Score 78.5;  DB 4;  Length 1409;
  Best Local Similarity   28.3%;  Pred. No. 23;
  Matches   34;  Conservative   12;  Mismatches   41;  Indels   33;  Gaps    5;

Qy         21 PGTPIPTFQLLPQNSLETTPSSVTSESSSGTTTG---PSASWSNSKASPYL--------- 68
              |  |: |  | |      ||   :|:  || :||   |  |  :| ||| |
Db       1269 PAHPVSTDSLAP---FTGTPGYFSSQPHSGNSTGSNLPRRSCPSSAASPTLQGPSDSPTS 1325

Qy         69 ------DTRVILSL--------DVPIGLLRILL----EQARYKAARNQAATNAQILAHVG 110
                    |  : |          :|  |  | |     : | |:|:|  | :|:|   | |
Db       1326 DSVSQSSTGTLSSTSFPQNSRSSLPSDLRTISLPSAGQSAVYQASRVSAVSNSQHYPHRG 1385


RESULT 15
Q9X6X6
ID   Q9X6X6      PRELIMINARY;      PRT;   889 AA.
AC   Q9X6X6;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Putative regulator YojN.
GN   YOJN.
OS   Salmonella typhimurium.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Salmonella.
OX   NCBI_TaxID=602;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LT2;
RA   Siano M.A., Mariconda S.E., Harshey R.M.;
RT   "Salmonella typhymurium homolog of yojN.";
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF153717; AAD34637.1; -.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0016301; F:kinase activity; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR003594; ATPbind_ATPase.
DR   InterPro; IPR005467; His_kinase.
DR   InterPro; IPR008207; Hpt.
DR   Pfam; PF02518; HATPase_c; 1.
DR   SMART; SM00387; HATPase_c; 1.
DR   SMART; SM00073; HPT; 1.
DR   PROSITE; PS50109; HIS_KIN; 1.
DR   PROSITE; PS50894; HPT; 1.
SQ   SEQUENCE   889 AA;  99795 MW;  4A10BD40EEC6D261 CRC64;

  Query Match             13.9%;  Score 77.5;  DB 2;  Length 889;
  Best Local Similarity   26.4%;  Pred. No. 17;
  Matches   33;  Conservative   18;  Mismatches   39;  Indels   35;  Gaps    5;

Qy         18 LFVPGTPIPTFQLLP-------QNSLETTPSSVTSE--------SSSGTTTGPSASWSNS 62
                 |  || |: :|:: |        ::| :  | |||           ||:  :||    |
Db       238 LIPPGMPLDSFRIEPDATQATGRSSEKEAPDSVTISFNGSKIEISSALNSTGMRLIWQVP 297

Qy         63 KASPYLDT--RVILSLDVPIGLLRILL--------------EQARYKAARNQ----AATN 102
                :  |||   ::| | : |||| : |              |     || |:      | |
Db       298 FGTLLLDTLQNILLPLLLNIGLLALALFGYATFRHQPGRSTESTSGNAANNELRVLRAIN 357

Qy        103 AQILA 107
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Db       358 EEIVS 362


Search completed: April 20, 2004, 18:56:42
Job time : 55.76 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 20, 2004, 18:53:13 ; Search time 24.64 Seconds
(without alignments)
234.664 Million cell updates/sec

Title: US-09-919-473-10
Perfect score: 557
Sequence: 1 MTRWALVVFVVLMLDRILFV.....KAARNQAATNAQILAHVGRR 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	179	32.1	38	4	US-09-799-978-43	Sequence 43, Appl
2	139	25.0	38	4	US-09-799-978-44	Sequence 44, Appl
3	76	13.6	542	4	US-09-189-462-6	Sequence 6, Appli
4	76	13.6	542	4	US-09-863-040-6	Sequence 6, Appli
5	72.5	13.0	526	2	US-08-853-659A-40	Sequence 40, Appl
6	71.5	12.8	308	4	US-09-252-991A-32516	Sequence 32516, A
7	71.5	12.8	410	4	US-09-252-991A-30606	Sequence 30606, A
8	71.5	12.8	465	1	US-08-471-496-9	Sequence 9, Appli
9	71.5	12.8	465	2	US-08-894-840-9	Sequence 9, Appli
10	71.5	12.8	465	3	US-09-139-675-9	Sequence 9, Appli
11	71.5	12.8	465	4	US-09-502-018-9	Sequence 9, Appli
12	71.5	12.8	521	1	US-08-063-552-2	Sequence 2, Appli
13	71.5	12.8	521	5	PCT-US93-05704-2	Sequence 2, Appli
14	71	12.7	422	4	US-09-252-991A-30314	Sequence 30314, A
15	70.5	12.7	1069	4	US-09-252-991A-24533	Sequence 24533, A
16	70	12.6	275	2	US-08-578-709-13	Sequence 13, Appl
17	70	12.6	390	4	US-09-489-039A-13547	Sequence 13547, A
18	70	12.6	425	4	US-09-489-039A-11016	Sequence 11016, A
19	70	12.6	500	2	US-08-578-709-15	Sequence 15, Appl
20	69	12.4	696	4	US-09-907-794A-91	Sequence 91, Appl
21	69	12.4	696	4	US-09-905-125A-91	Sequence 91, Appl
22	69	12.4	696	4	US-09-902-775A-91	Sequence 91, Appl
23	68.5	12.3	171	5	PCT-US95-04910-12	Sequence 12, Appl
24	68	12.2	124	3	US-08-981-189B-15	Sequence 15, Appl
25	68	12.2	1025	4	US-09-711-164-443	Sequence 443, App
26	67.5	12.1	582	3	US-08-906-865-3	Sequence 3, Appli
27	67.5	12.1	582	4	US-09-129-668-3	Sequence 3, Appli
28	67.5	12.1	681	3	US-08-760-615-6	Sequence 6, Appli
29	67.5	12.1	915	4	US-09-489-039A-8249	Sequence 8249, Ap
30	67	12.0	498	2	US-08-942-218A-3	Sequence 3, Appli
31	67	12.0	548	3	US-08-942-001-2	Sequence 2, Appli
32	67	12.0	548	3	US-09-337-386-2	Sequence 2, Appli
33	67	12.0	548	4	US-09-846-922-2	Sequence 2, Appli
34	67	12.0	1337	3	US-08-854-585-2	Sequence 2, Appli
35	67	12.0	1337	4	US-09-447-533-2	Sequence 2, Appli
36	67	12.0	1337	5	PCT-US95-05512-2	Sequence 2, Appli
37	66.5	11.9	562	4	US-09-328-352-4694	Sequence 4694, Ap
38	66	11.8	1048	4	US-09-171-699-10	Sequence 10, Appl
39	65.5	11.8	238	4	US-09-149-476-485	Sequence 485, App
40	65.5	11.8	332	4	US-09-252-991A-32526	Sequence 32526, A
41	65.5	11.8	515	1	US-08-063-552-4	Sequence 4, Appli
42	65.5	11.8	515	5	PCT-US93-05704-4	Sequence 4, Appli
43	65	11.7	145	4	US-09-252-991A-28281	Sequence 28281, A
44	65	11.7	610	1	US-07-821-717B-6	Sequence 6, Appli
45	65	11.7	610	1	US-08-119-262B-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-799-978-43
; Sequence 43, Application US/09799978
; Patent No. 6670140
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert
; APPLICANT: Sheldon, Russell
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or
; TITLE OF INVENTION: Function Using Corticotropin Releasing Factor Receptors
; FILE REFERENCE: 8448
; CURRENT APPLICATION NUMBER: US/09/799,978
; CURRENT FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-799-978-43

Query Match 32.1%; Score 179; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 2e-14;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         72 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 109
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Db          1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
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RESULT 2
US-09-799-978-44
; Sequence 44, Application US/09799978
; Patent No. 6670140
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert
; APPLICANT: Sheldon, Russell
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or
; TITLE OF INVENTION: Function Using Corticotropin Releasing Factor Receptors
; FILE REFERENCE: 8448
; CURRENT APPLICATION NUMBER: US/09/799,978
; CURRENT FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-978-44

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  Query Match             25.0%;  Score 139;  DB 4;  Length 38;
  Best Local Similarity   76.3%;  Pred. No. 1.2e-09;
  Matches   29;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         72 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 109
              ::|||||||||:|||||| :||| || |||:||| |
Db          1 IVLSLDVPIGLLQILLEQARARAAREQATTNARILARV 38


RESULT 3
US-09-189-462-6
; Sequence 6, Application US/09189462
; Patent No. 6303302
; GENERAL INFORMATION:
;  APPLICANT: Rupp, Steffan
;  APPLICANT: Roberson, Laura
;  APPLICANT: Summers, Eric F.
;  APPLICANT: Hecht, Peter
;  APPLICANT: Roberts, Radclyffe
;  APPLICANT: Madhani, Hiran
;  APPLICANT: Styles, Cora Ann
;  APPLICANT: Lo, Hsiu-Jung
;  APPLICANT: Sherman, Amir
;  APPLICANT: Cali, Brian
;  APPLICANT: Fink, Gerald
;  TITLE OF INVENTION: REGULATION OF FUNGAL GENE EXPRESSION
;  FILE REFERENCE: 50078/003002
;  CURRENT APPLICATION NUMBER: US/09/189,462
;  CURRENT FILING DATE: 1998-11-10
;  EARLIER APPLICATION NUMBER: 60/066,129
;  EARLIER FILING DATE: 1997-11-19
;  EARLIER APPLICATION NUMBER: 60/066,308
;  EARLIER FILING DATE: 1997-11-21
;  EARLIER APPLICATION NUMBER: 60/066,462
;  EARLIER FILING DATE: 1997-11-24
;  EARLIER APPLICATION NUMBER: 60/078,610
;  EARLIER FILING DATE: 1998-03-19
;  EARLIER APPLICATION NUMBER: 60/094,523
;  EARLIER FILING DATE: 1998-07-29
;  NUMBER OF SEQ ID NOS: 67
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 542
;   TYPE: PRT
;   ORGANISM: Saccharomyces cerevisiae
US-09-189-462-6

  Query Match             13.6%;  Score 76;  DB 4;  Length 542;
  Best Local Similarity   40.0%;  Pred. No. 1.5;
  Matches   18;  Conservative    7;  Mismatches   20;  Indels    0;  Gaps    0;

Qy         35 SLETTPSSVTSESSSGTTTGPSASWSNSKASPYLDTRVILSLDVP 79
              | |   || |  :    ||:  |:|  ||| ||   :  | :|:|:|
Db        226 STEDESSSYTQLTQKSTTSNSSSSSVNSKTSPLPNKTVTISVDIP 270


RESULT 4
US-09-863-040-6
; Sequence 6, Application US/09863040
; Patent No. 6599705
; GENERAL INFORMATION:
;  APPLICANT: Rupp, Steffan
;  APPLICANT:  Robertson, Laura
;  APPLICANT:  Summers, Eric F.
;  APPLICANT:  Hecht, Peter
;  APPLICANT:  Roberts, Radclyffe
;  APPLICANT:  Madhani, Hiren
;  APPLICANT:  Styles, Cora Ann
;  APPLICANT:  Lo, Hsiu-Jung
;  APPLICANT:  Sherman, Amir
;  APPLICANT:  Cali, Brian
;  APPLICANT:  Fink, Gerald R.
;  TITLE OF INVENTION: Regulation of Fungal Gene Expression
;  FILE REFERENCE: 109272.152
;  CURRENT APPLICATION NUMBER: US/09/863,040
;  CURRENT FILING DATE:  2001-05-22
;  PRIOR APPLICATION NUMBER: US 60/066,129
;  PRIOR FILING DATE: 1997-11-19
;  PRIOR APPLICATION NUMBER: US 60/066,308
;  PRIOR FILING DATE: 1997-11-21
;  PRIOR APPLICATION NUMBER: US 60/066,462
;  PRIOR FILING DATE: 1997-11-24
;  PRIOR APPLICATION NUMBER: US 60/078,610
;  PRIOR FILING DATE: 1998-03-19
;  PRIOR APPLICATION NUMBER: US 60/094,523
;  PRIOR FILING DATE: 1998-07-29
;  NUMBER OF SEQ ID NOS: 67
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 542
;   TYPE: PRT
;   ORGANISM: Saccharomyces cerevisiae INV9
US-09-863-040-6

  Query Match             13.6%;  Score 76;  DB 4;  Length 542;
  Best Local Similarity   40.0%;  Pred. No. 1.5;
  Matches   18;  Conservative    7;  Mismatches   20;  Indels    0;  Gaps    0;

Qy         35 SLETTPSSVTSESSSGTTTGPSASWSNSKASPYLDTRVILSLDVP 79
              | |   || |  :    ||:  |:|  ||| ||   :  | :|:|:|
Db        226 STEDESSSYTQLTQKSTTSNSSSSSVNSKTSPLPNKTVTISVDIP 270


RESULT 5
US-08-853-659A-40
; Sequence 40, Application US/08853659A
; Patent No. 5925522
;  GENERAL INFORMATION:
;    APPLICANT:  Wong, K.K.; Saffer, J.D.
;    TITLE OF INVENTION:  A Salmonella Sequence, Methods Of Detection
;    TITLE OF INVENTION:  Of A
;    TITLE OF INVENTION:  Salmonella Sequence, And Methods Of Detection Of Salmonella
;    NUMBER OF SEQUENCES:  67
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Paul W. Zimmerman
;      ADDRESSEE:  Intellectual Property Services
;      ADDRESSEE:  Battelle Memorial Institute
;      ADDRESSEE:  PNNL P.O. Box 999
;      STREET:  Washington Way
;      CITY:  Richland
;      STATE:  Washington
;      COUNTRY:  U.S.A.
;      ZIP:  99352
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette 3.50", 1.44 Mb storage
;      COMPUTER:  IBM PC/XT/AT
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Word Processor (WordPerfect 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/853,659A
;      FILING DATE:  Unknown
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  none
;      FILING DATE:  n/a
;  INFORMATION FOR SEQ ID NO:  40:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  526 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-853-659A-40

  Query Match             13.0%;  Score 72.5;  DB 2;  Length 526;
  Best Local Similarity   29.2%;  Pred. No. 3.8;
  Matches   21;  Conservative   14;  Mismatches   22;  Indels   15;  Gaps    3;
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```
Qy          10 VVLMLDRILFVPGTPIPTFQLLPQNSLETTPSSVTSESSSGTTTGPS---ASWSNSKASP 66
               :|: :| :      |  |||:| |:       |||:       |  ||    :  |:|
Db         162 LVITIDSV-----TDKPTFELSPE-------SSVSGHKGLTPTLTPSIVGTAEENAKVDI 209

Qy          67 YLDTRVILSLDV 78
               |:| ::: |:||
Db         210 YVDNKLVASVDV 221
```

RESULT 6
US-09-252-991A-32516
; Sequence 32516, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32516
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32516

Query Match 12.8%; Score 71.5; DB 4; Length 308;
Best Local Similarity 35.6%; Pred. No. 2.4;
Matches 26; Conservative 11; Mismatches 27; Indels 9; Gaps 4;

```
Qy          32 PQNSLETTPSSVTSESSSGTTTGPSASWSNSKASPYLDTRVILSLDVPIGLLRILLEQAR 91
               | :|||  ||  || ::: | | ||::|       |  |:  |: ||    | :|   |
Db         173 PISSLEVCPS--TSANTTPTATLPSSTW----LQDVLARRICASVRVP-SRTRRMLGSPR 225

Qy          92 YKAARNQAATNAQ 104
               |   :| | : ||
Db         226 YH--QNIAGSTAQ 236
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RESULT 7
US-09-252-991A-30606
; Sequence 30606, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30606
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30606

Query Match 12.8%; Score 71.5; DB 4; Length 410;
Best Local Similarity 27.0%; Pred. No. 3.5;
Matches 27; Conservative 13; Mismatches 37; Indels 23; Gaps 4;

```
Qy          21 PGT-PIPT--FQLLPQNSLETTPSSVTSESSSGTTTGPSASWSNSKASPYLDTRVILSLD 77
               ||  |||:  ||  |:  |   | :  : : :    |  |    :: :|
```

```
Db           9 PGDGPIPSEMFQQAPRGFLAAEPGAFDAAAGAPVAAGVDAQVGIAEGAPL---------- 58

Qy          78 VPIGLLRILLEQA--------RYKAARNQAATNAQILAHV 109
                  :|| |  :| |        || || :     ||:| ||
Db          59 --VGLRRACIEPAVGDAEGGFRYGAADHFGEGAAQVLDHV 96
```

RESULT 8
US-08-471-496-9
; Sequence 9, Application US/08471496
; Patent No. 5798223
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; APPLICANT: CAO, LIANG
; APPLICANT: ROSEN, CRAIG
; TITLE OF INVENTION: HUMAN AMINE TRANSPORTER
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,496
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US95/02645
; FILING DATE: 01-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0830001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 465 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-471-496-9

Query Match 12.8%; Score 71.5; DB 1; Length 465;
Best Local Similarity 33.3%; Pred. No. 4.2;
Matches 22; Conservative 8; Mismatches 25; Indels 11; Gaps 2;

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Qy           6 LVVFVVLMLDRILFVPGTPI-PTFQLLPQNSLETTPSSVTSESSSGTTTGPSASWSNSKA 64
               :|||| |:|| :|     || |||           ::   :|:|    |||  |   :
Db          25 VVVFVALLLDNMLLTVVVPIVPTFLY----------ATEPKDSNSSLHRGPSVSSQQALT 74

Qy          65 SPYLDT 70
               ||   |
Db          75 SPAFST 80
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RESULT 9
US-08-894-840-9
; Sequence 9, Application US/08894840
; Patent No. 5859200
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; APPLICANT: CAO, LIANG
; APPLICANT: ROSEN, CRAIG A.

```
;    TITLE OF INVENTION:  HUMAN AMINE TRANSPORTER
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVENUE, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/894,840
;      FILING DATE:  29-AUG-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  STEFFE, ERIC K
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0830000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  465 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-894-840-9

  Query Match             12.8%;  Score 71.5;  DB 2;  Length 465;
  Best Local Similarity   33.3%;  Pred. No. 4.2;
  Matches   22;  Conservative    8;  Mismatches   25;  Indels   11;  Gaps    2;

Qy          6 LVVFVVLMLDRILFVPGTPI-PTFQLLPQNSLETTPSSVTSESSSGTTTGPSASWSNSKA 64
              :|||| |:|| :|     || |||           ::   :|:|    ||| |   :
Db         25 VVVFVALLLDNMLLTVVVPIVPTFLY----------ATEFKDSNSSLHRGPSVSSQQALT 74

Qy         65 SPYLDT 70
              ||   |
Db         75 SPAFST 80


RESULT 10
US-09-139-675-9
; Sequence 9, Application US/09139675A
; Patent No. 6117426
; GENERAL INFORMATION:
;  APPLICANT: Li, Yi
;  APPLICANT: Cao, Liang
;  APPLICANT: Rosen, Craig
;  TITLE OF INVENTION: Human Amine Transporter
;  FILE REFERENCE: 1488.0830003
;  CURRENT APPLICATION NUMBER: US/09/139,675A
;  CURRENT FILING DATE: 1998-08-25
;  EARLIER APPLICATION NUMBER: WO PCT/US95/02645
;  EARLIER FILING DATE: 1995-03-01
;  EARLIER APPLICATION NUMBER: US 08/471,496
;  EARLIER FILING DATE: 1995-06-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Rattus sp.
US-09-139-675-9

  Query Match             12.8%;  Score 71.5;  DB 3;  Length 465;
  Best Local Similarity   33.3%;  Pred. No. 4.2;
  Matches   22;  Conservative    8;  Mismatches   25;  Indels   11;  Gaps    2;

Qy          6 LVVFVVLMLDRILFVPGTPI-PTFQLLPQNSLETTPSSVTSESSSGTTTGPSASWSNSKA 64
              :|||| |:|| :|     || |||           ::   :|:|    ||| |   :
Db         25 VVVFVALLLDNMLLTVVVPIVPTFLY----------ATEFKDSNSSLHRGPSVSSQQALT 74

Qy         65 SPYLDT 70
              ||   |
Db         75 SPAFST 80


RESULT 11
US-09-502-018-9
; Sequence 9, Application US/09502018
; Patent No. 6630443
; GENERAL INFORMATION:
;  APPLICANT: Li, Yi
;  APPLICANT:  Cao, Liang
;  APPLICANT:  Rosen, Craig
;  TITLE OF INVENTION: Human Amine Transporter
;  FILE REFERENCE: 1488.0830003
;  CURRENT APPLICATION NUMBER: US/09/502,018
;  CURRENT FILING DATE:  2000-02-11
;  PRIOR APPLICATION NUMBER: US/09/139,675
;  PRIOR FILING DATE: 1998-08-25
;  PRIOR APPLICATION NUMBER: WO PCT/US95/02645
;  PRIOR FILING DATE: 1995-03-01
;  PRIOR APPLICATION NUMBER: US 08/471,496
;  PRIOR FILING DATE: 1995-06-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Rattus sp.
US-09-502-018-9

  Query Match             12.8%;  Score 71.5;  DB 4;  Length 465;
  Best Local Similarity   33.3%;  Pred. No. 4.2;
  Matches   22;  Conservative    8;  Mismatches   25;  Indels   11;  Gaps    2;

Qy          6 LVVFVVLMLDRILFVPGTPI-PTFQLLPQNSLETTPSSVTSESSSGTTTGPSASWSNSKA 64
              :|||| |:|| :|     || |||           ::   :|:|    ||| |   :
Db         25 VVVFVALLLDNMLLTVVVPIVPTFLY----------ATEFKDSNSSLHRGPSVSSQQALT 74

Qy         65 SPYLDT 70
              ||   |
Db         75 SPAFST 80


RESULT 12
US-08-063-552-2
; Sequence 2, Application US/08063552
; Patent No. 5688936
;  GENERAL INFORMATION:
;    APPLICANT:  Edwards, Robert H
;    TITLE OF INVENTION:  Vesicle Membrane Transport Proteins
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheldon & Mak
;      STREET:  225 South Lake Avenue, Ninth Floor
;      CITY:  Pasadena
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/063,552
;      FILING DATE:  19930514
;      CLASSIFICATION:  530
```

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;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Farber, Michael B
;      REGISTRATION NUMBER:  32,612
;      REFERENCE/DOCKET NUMBER:  9067-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (818) 796-4000
;      TELEFAX:  (818) 795-6321
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  521 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-063-552-2

  Query Match             12.8%;  Score 71.5;  DB 1;  Length 521;
  Best Local Similarity   33.3%;  Pred. No. 4.9;
  Matches   22;  Conservative    8;  Mismatches   25;  Indels   11;  Gaps    2;

Qy          6 LVVFVVLMLDRILFVPGTPI-PTFQLLPQNSLETTPSSVTSESSSGTTTGPSASWSNSKA 64
              :|||| |:|| :|    || |||           ::   :|:|    ||| |   :
Db         25 VVVFVALLLDNMLLTVVVPIVPTFLY----------ATEFKDSNSSLHRGPSVSSQQALT 74

Qy         65 SPYLDT 70
              ||   |
Db         75 SPAFST 80


RESULT 13
PCT-US93-05704-2
; Sequence 2, Application PC/TUS9305704
;  GENERAL INFORMATION:
;    APPLICANT:  Edwards, Robert H
;    TITLE OF INVENTION:  Vesicle Membrane Transport Proteins
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheldon & Mak
;      STREET:  225 South Lake Avenue, Ninth Floor
;      CITY:  Pasadena
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/05704
;      FILING DATE:  19930611
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Farber, Michael B
;      REGISTRATION NUMBER:  32,612
;      REFERENCE/DOCKET NUMBER:  9067-1PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (818) 796-4000
;      TELEFAX:  (818) 795-6321
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  521 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US93-05704-2

  Query Match             12.8%;  Score 71.5;  DB 5;  Length 521;
  Best Local Similarity   33.3%;  Pred. No. 4.9;
  Matches   22;  Conservative    8;  Mismatches   25;  Indels   11;  Gaps    2;

Qy          6 LVVFVVLMLDRILFVPGTPI-PTFQLLPQNSLETTPSSVTSESSSGTTTGPSASWSNSKA 64
              :|||| |:|| :|    || |||           ::   :|:|    ||| |   :
Db         25 VVVFVALLLDNMLLTVVVPIVPTFLY----------ATEFKDSNSSLHRGPSVSSQQALT 74

Qy         65 SPYLDT 70
              ||   |
Db         75 SPAFST 80


RESULT 14
US-09-252-991A-30314
; Sequence 30314, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 30314
;   LENGTH: 422
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30314

  Query Match             12.7%;  Score 71;  DB 4;  Length 422;
  Best Local Similarity   25.0%;  Pred. No. 4.2;
  Matches   18;  Conservative   16;  Mismatches   38;  Indels    0;  Gaps    0;

Qy         40 PSSVTSESSSGTTTGPSASWSNSKASPYLDTRVILSLDVPIGLLRILLEQARYKAARNQA 99
              |::  :   :| | | |    ::   | : :|    | ||  | ::  :| | : |
Db         11 PAATAAIPRAGATRGCSGPGRSATGRPSMASRRSAPLPVPEELRQVARQQQRQQQAEQAE 70

Qy        100 ATNAQILAHVGR 111
                :|::| |: |
Db         71 QASARVLRHLDR 82


RESULT 15
US-09-252-991A-24533
; Sequence 24533, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 24533
;   LENGTH: 1069
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24533

  Query Match             12.7%;  Score 70.5;  DB 4;  Length 1069;
  Best Local Similarity   27.1%;  Pred. No. 17;
  Matches   39;  Conservative   13;  Mismatches   35;  Indels   57;  Gaps    7;

Qy          5 ALVVFVVLMLDRILF-------VPGTPIPTFQ---LLPQNSLETTPSSV----------- 43
              ||:    :|  :  |       :|    || |   |||  | ||  |||
Db         52 ALLTLASLLLGLLAFLRLGVAPLPEADFPTIQINALLPGGSPETMASSVATPLEVQFSAI 111

Qy         44 ------TSESSSGTTTGPSASWSNSKA---------------------SPYLDT-RVIL 74
                   || |: ||||  :  :|  |:                       | | | | :
```

```
Db        112 PGITEMTSSSALGTTT-LTLQFSLDKSIDVAAQEVQAAINAAAGRLPVDMPNLPTWRKVN 170

Qy         75 SLDVPIGLLRI------LLEQARY 92
                | || :||:      |:| : |
Db        171 PADSPIMILRVNSEMMPLIELSDY 194
```

Search completed: April 20, 2004, 18:58:16
Job time : 35.64 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 20, 2004, 18:51:32 ; Search time 14.9333 Seconds
(without alignments)
390.526 Million cell updates/sec

Title: US-09-919-473-10
Perfect score: 557
Sequence: 1 MTRWALVVFVVLMLDRILFV.....KAARNQAATNAQILAHVGRR 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	557	100.0	112	1	UCN2_MOUSE	Q99ml8 mus musculu
2	482.5	86.6	109	1	UCN2_RAT	Q91ww1 rattus norv
3	312	56.0	112	1	UCN2_HUMAN	Q96rp3 homo sapien
4	100.5	18.0	164	1	UCN3_MOUSE	Q924a4 mus musculu
5	99	17.8	161	1	UCN3_HUMAN	Q969e3 homo sapien
6	79	14.2	539	1	STG2_HUMAN	Q9ny99 homo sapien
7	76	13.6	837	1	MUCL_RAT	P98089 rattus norv
8	75.5	13.6	2090	1	N214_HUMAN	P35658 homo sapien
9	74.5	13.4	196	1	CRF_HUMAN	P06850 homo sapien
10	71.5	12.8	222	1	VV_SV5	P11207 simian viru
11	71.5	12.8	436	1	GCM1_MOUSE	P70348 mus musculu
12	71.5	12.8	519	1	AB31_ARATH	Q9fyl3 arabidopsis
13	71.5	12.8	521	1	VMT1_RAT	Q01818 rattus norv
14	71	12.7	1367	1	AMYH_YEAST	P08640 saccharomyc
15	70.5	12.7	392	1	RRPP_SV5	P11208 simian viru
16	70.5	12.7	4377	1	ANK3_HUMAN	Q12955 homo sapien
17	70	12.6	145	1	UR1_CARAU	Q9ptq4 carassius a
18	70	12.6	500	1	PTGI_HUMAN	Q16647 homo sapien
19	70	12.6	519	1	MS2P_HUMAN	O43462 homo sapien
20	69.5	12.5	187	1	CRF_RAT	P01143 rattus norv
21	69.5	12.5	636	1	YNR6_YEAST	P53882 saccharomyc
22	69	12.4	539	1	STG2_MOUSE	Q925e0 mus musculu
23	68.5	12.3	324	1	NAA2_RHILO	Q982f2 rhizobium l
24	68.5	12.3	395	1	PER_DROEQ	P92203 drosophila
25	68.5	12.3	532	1	VAT_HUMAN	Q16572 homo sapien
26	68.5	12.3	743	1	TFE3_HUMAN	P19532 homo sapien
27	68	12.2	122	1	UCN1_MOUSE	P81615 mus musculu
28	68	12.2	122	1	UCN1_RAT	P55090 rattus norv
29	68	12.2	124	1	UCN1_HUMAN	P55089 homo sapien
30	68	12.2	145	1	UR1_CYPCA	P01146 cyprinus ca
31	68	12.2	162	1	CRF1_CATCO	P13241 catostomus
32	68	12.2	165	1	UR1_ONCMY	O93448 oncorhynchu
33	68	12.2	254	1	YMH1_CAEEL	P34468 caenorhabdi
34	68	12.2	469	1	VL2_HPVME	P27965 human papil
35	68	12.2	605	1	WSC4_YEAST	P38739 saccharomyc
36	68	12.2	681	1	YDHE_SCHPO	Q92359 schizosacch
37	68	12.2	830	1	PKN2_MYXXA	P54736 myxococcus
38	68	12.2	1025	1	YEGO_ECOLI	P76399 escherichia
39	68	12.2	1609	1	FIG2_YEAST	P25653 saccharomyc
40	67.5	12.1	536	1	YEN1_SCHPO	O13695 schizosacch
41	67.5	12.1	582	1	SYN2_HUMAN	Q92777 homo sapien
42	67.5	12.1	750	1	CTPB_MYCLE	P46840 mycobacteri
43	67.5	12.1	794	1	KI11_HUMAN	Q8tdc3 homo sapien
44	67	12.0	234	1	MAG8_HUMAN	P43361 homo sapien
45	67	12.0	417	1	GP61_HUMAN	Q9bzj8 homo sapien

ALIGNMENTS

RESULT 1
UCN2_MOUSE
ID UCN2_MOUSE STANDARD; PRT; 112 AA.
AC Q99ML8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Urocortin II precursor (Ucn II).
GN UCN2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=21126973; PubMed=11226328;
RA Reyes T.M., Lewis K., Perrin M.H., Kunitake K.S., Vaughan J.,
RA Arias C.A., Hogenesch J.B., Gulyas J., Rivier J., Vale W.W.,
RA Sawchenko P.E.;
RT "Urocortin II: A member of the corticotropin-releasing factor (CRF)
RT neuropeptide family that is selectively bound by type 2 CRF
RT receptors.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:2843-2848(2001).
CC -!- FUNCTION: Suppress food intake, delays gastric emptying and
CC decreases heat-induced edema. Might represent an endogenous ligand
CC for maintaining homeostasis after stress (By similarity).
CC -!- SUBUNIT: Binds with high affinity to CRF receptors 2-alpha and 2-
CC beta (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing
CC factor/urotensin I family.
CC ---

CC ---
DR EMBL; AF331517; AAK16157.1; -.
DR MGD; MGI:2176375; Ucn2.
DR GO; GO:0005576; C:extracellular; ISS.
DR GO; GO:0005102; F:receptor binding; ISS.
DR GO; GO:0006171; P:cAMP biosynthesis; ISS.
DR GO; GO:0007586; P:digestion; ISS.
DR GO; GO:0006950; P:response to stress; ISS.
KW Hormone; Amidation; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 20 70 POTENTIAL.
FT CHAIN 72 112 UROCORTIN II.
SQ SEQUENCE 112 AA; 12179 MW; C871002CDAA64FB7 CRC64;

Query Match 100.0%; Score 557; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.4e-46;

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  Matches  112;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MTRWALVVFVVLMLDRILFVPGTPIPTFQLLPQNSLETTPSSVTSESSSGTTTGPSASWS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MTRWALVVFVVLMLDRILFVPGTPIPTFQLLPQNSLETTPSSVTSESSSGTTTGPSASWS 60

Qy         61 NSKASPYLDTRVILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHVGRR 112
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NSKASPYLDTRVILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHVGRR 112


RESULT 2
UCN2_RAT
ID   UCN2_RAT       STANDARD;      PRT;   109 AA.
AC   Q91WW1;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Urocortin II precursor (Ucn II).
GN   UCN2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Midbrain;
RA   Park J.H., Ju S.K., Lee M.K.;
RT   "Cloning and analysis of tissue-specific mRNA expression of rat
RT   urocortin II.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Suppress food intake, delays gastric emptying and
CC       decreases heat-induced edema. Might represent an endogenous ligand
CC       for maintaining homeostasis after stress (By similarity).
CC   -!- SUBUNIT: Binds with high affinity to CRF receptors 2-alpha and 2-
CC       beta (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing
CC       factor/urotensin I family.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AY044835; AAK98780.1; -.
DR   GO; GO:0005576; C:extracellular; ISS.
DR   GO; GO:0005102; F:receptor binding; ISS.
DR   GO; GO:0006171; P:cAMP biosynthesis; ISS.
DR   GO; GO:0007586; P:digestion; ISS.
DR   GO; GO:0006950; P:response to stress; ISS.
DR   InterPro; IPR000187; corticoliberin.
DR   SMART; SM00039; CRF; 1.
KW   Hormone; Amidation; Signal.
FT   SIGNAL       1     19       POTENTIAL.
FT   PROPEP      20     67       POTENTIAL.
FT   CHAIN       69    109       UROCORTIN II.
SQ   SEQUENCE   109 AA;  11922 MW;  AA2B46D8903ED83E CRC64;

  Query Match             86.6%;  Score 482.5;  DB 1;  Length 109;
  Best Local Similarity   90.2%;  Pred. No. 1.7e-39;
  Matches  101;  Conservative    2;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          1 MTRWALVVFVVLMLDRILFVPGTPIPTFQLLPQNSLETTPSSVTSESSSGTTTGPSASWS 60
              |||||||||:||||||   |||||||||||||||  |||||||:||| | ||||||||||
Db          1 MTRWALVVFMVLMLDR---VPGTPIPTFQLLPQNYPETTPSSVSSESPSDTTTGPSASWS 57

Qy         61 NSKASPYLDTRVILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHVGRR 112
              |||||||||||||||||||||||||||| |||||||||||||||| ||||
Db         58 NSKASPYLDTRVILSLDVPIGLLRILLEQARNKAARNQAATNAQILARVGRR 109
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RESULT 3
UCN2_HUMAN
ID   UCN2_HUMAN     STANDARD;      PRT;   112 AA.
AC   Q96RP3; Q9BUG0;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Urocortin II precursor (Ucn II) (Stresscopin-related peptide)
DE   (Urocortin-related peptide).
GN   UCN2 OR SRP OR URP.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21227098; PubMed=11329063;
RA   Hsu S.Y., Hsueh A.J.W.;
RT   "Human stresscopin and stresscopin-related peptide are selective
RT   ligands for the type 2 corticotropin-releasing hormone receptor.";
RL   Nat. Med. 7:605-611(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skin, and Uterus;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Suppress food intake, delays gastric emptying and
CC       decreases heat-induced edema. Might represent an endogenous ligand
CC       for maintaining homeostasis after stress.
CC   -!- SUBUNIT: Binds with high affinity to CRF receptors 2-alpha and 2-
CC       beta.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing
CC       factor/urotensin I family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF320560; AAK52672.1; -.
DR   EMBL; BC002647; AAH02647.2; -.
DR   EMBL; BC022096; AAH22096.1; -.
DR   MIM; 605902; -.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0005102; F:receptor binding; IPI.
DR   GO; GO:0006171; P:cAMP biosynthesis; IEP.
DR   GO; GO:0007586; P:digestion; NAS.
DR   GO; GO:0006950; P:response to stress; NAS.
```

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DR   InterPro; IPR000187; corticoliberin.
DR   SMART; SM00039; CRF; 1.
KW   Hormone; Amidation; Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   PROPEP       20     70       POTENTIAL.
FT   CHAIN        72    112       UROCORTIN II.
SQ   SEQUENCE   112 AA;  12146 MW;  0EFF29A3463723D4 CRC64;

  Query Match             56.0%;  Score 312;  DB 1;  Length 112;
  Best Local Similarity   60.9%;  Pred. No. 3.5e-23;
  Matches   67;  Conservative   15;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          1 MTRWALVVFVVLMLDRILFVPGTPIPTFQLLPQNSLETTPSSVTSESSSGTTTGPSASWS 60
              ||| ||:: :|||| |:| || |||||||| |||| :|||    ||| |   | | |: |
Db          1 MTRCALLLLMVLMLGRVLVVPVTPIPTFQLRPQNSPQTTPRPAASESPSAAPTWPWAAQS 60

Qy         61 NSKASPYLDTRVILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHVG 110
              :   : :  :|::||||||||||:|||||| :||| || |||:||| ||
Db         61 HCSPTRHPGSRIVLSLDVPIGLLQILLEQARARAAREQATTNARILARVG 110


RESULT 4
UCN3_MOUSE
ID   UCN3_MOUSE     STANDARD;      PRT;   164 AA.
AC   Q924A4;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Urocortin III precursor (Ucn III).
GN   UCN3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A., SYNTHESIS OF UCN III, AND TISSUE SPECIFICITY.
RX   MEDLINE=21310014; PubMed=11416224;
RA   Lewis K., Li C., Perrin M.H., Blount A., Kunitake K., Donaldson C.,
RA   Vaughan J., Reyes T.M., Gulyas J., Fischer W., Bilezikjian L.,
RA   Rivier J., Sawchenko P.E., Vale W.W.;
RT   "Identification of urocortin III, an additional member of the
RT   corticotropin-releasing factor (CRF) family with high affinity for the
RT   CRF2 receptor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:7570-7575(2001).
CC   -!- FUNCTION: Suppress food intake, delays gastric emptying and
CC       decreases heat-induced edema. Might represent an endogenous ligand
CC       for maintaining homeostasis after stress (By similarity).
CC   -!- SUBUNIT: Binds with high affinity to CRF receptors 2-alpha and 2-
CC       beta.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Expressed in some areas of the brain including
CC       the hypothalamus, amygdala, and brainstem, but is not evident in
CC       the cerebellum, pituitary, or cerebral cortex; it is also
CC       expressed peripherally in small intestine and skin.
CC   -!- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing
CC       factor/urotensin I family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF361944; AAK67318.1; -.
DR   MGD; MGI:1932970; Ucn3.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0007189; P:G-protein signaling, adenylate cyclase acti. . .; IDA.
KW   Hormone; Amidation; Signal.
FT   SIGNAL        1     23       POTENTIAL.
FT   PROPEP       24    121
FT   CHAIN       123    160       UROCORTIN III.
FT   MOD_RES     160    160       AMIDATION (G-161 PROVIDE AMIDE GROUP).
SQ   SEQUENCE   164 AA;  18063 MW;  93A77CB93DA56E5C CRC64;

  Query Match             18.0%;  Score 100.5;  DB 1;  Length 164;
  Best Local Similarity   31.0%;  Pred. No. 0.0089;
  Matches   26;  Conservative   16;  Mismatches   35;  Indels    7;  Gaps    1;

Qy         36 LETTPSSVTSESSSGTTTGPSASWSNSKASPYLD-------TRVILSLDVPIGLLRILLE 88
              :: | |      : :|:|     | :  |   | |       |:  |||||  :: ||
Db         80 IKRTFSGAAGGNGAGSTRYRYQSQAQHKGKLYPDKPKSDRGTKFTLSLDVPTNIMNILFN 139

Qy         89 QARYKAARNQAATNAQILAHVGRR 112
                : |  | :|| |||::| :|::
Db        140 IDKAKNLRAKAAANAQLMAQIGKK 163


RESULT 5
UCN3_HUMAN
ID   UCN3_HUMAN     STANDARD;      PRT;   161 AA.
AC   Q969E3;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Urocortin III precursor (Ucn III) (Stresscopin).
GN   UCN3 OR SPC.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND SYNTHESIS OF UCN III.
RX   MEDLINE=21310014; PubMed=11416224;
RA   Lewis K., Li C., Perrin M.H., Blount A., Kunitake K., Donaldson C.,
RA   Vaughan J., Reyes T.M., Gulyas J., Fischer W., Bilezikjian L.,
RA   Rivier J., Sawchenko P.E., Vale W.W.;
RT   "Identification of urocortin III, an additional member of the
RT   corticotropin-releasing factor (CRF) family with high affinity for the
RT   CRF2 receptor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:7570-7575(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21227098; PubMed=11329063;
RA   Hsu S.Y., Hsueh A.J.W.;
RT   "Human stresscopin and stresscopin-related peptide are selective
RT   ligands for the type 2 corticotropin-releasing hormone receptor.";
RL   Nat. Med. 7:605-611(2001).
CC   -!- FUNCTION: Suppress food intake, delays gastric emptying and
CC       decreases heat-induced edema. Might represent an endogenous ligand
CC       for maintaining homeostasis after stress.
CC   -!- SUBUNIT: Binds with high affinity to CRF receptors 2-alpha and 2-
CC       beta.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing
CC       factor/urotensin I family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF361943; AAK67317.1; -.
DR   EMBL; AY026949; AAK11729.1; -.
DR   Genew; HGNC:17781; UCN3.
DR   MIM; 605901; -.
KW   Hormone; Amidation; Signal.
FT   SIGNAL        1     21       POTENTIAL.
FT   PROPEP       22    118
FT   CHAIN       120    157       UROCORTIN III.
FT   MOD_RES     157    157       AMIDATION (G-158 PROVIDE AMIDE GROUP).
SQ   SEQUENCE   161 AA;  17862 MW;  F92B2C8C3087857D CRC64;
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  Query Match             17.8%;  Score 99;  DB 1;  Length 161;
  Best Local Similarity   32.5%;  Pred. No. 0.012;
  Matches   27;  Conservative   14;  Mismatches   34;  Indels    8;  Gaps    2;

Qy         37 ETTPSSVTSESSSGTTTGPSASWSNSKASPYLD-------TRVILSLDVPIGLLRILLEQ 89
              :| | |  :   :| |     | :  :  | |          |:  ||||||  :: :|
Db         79 KTFPIS-GARGGAGGTRYRYVSQAQPRGKPRQDTAKSPHRTKFTLSLDVPTNIMNLLFNI 137

Qy         90 ARYKAARNQAATNAQILAHVGRR 112
              |: |  | ||| || ::| :||:
Db        138 AKAKNLRAQAAANAHLMAQIGRK 160


RESULT 6
STG2_HUMAN
ID   STG2_HUMAN      STANDARD;      PRT;   539 AA.
AC   Q9NY99;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Gamma-2-syntrophin (G2SYN) (Syntrophin 5) (SYN5).
GN   SNTG2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND INTERACTION WITH DMD; DTNA
RP   AND DTNB.
RC   TISSUE=Fetal brain, and Neuron;
RX   MEDLINE=20283612; PubMed=10747910;
RA   Piluso G., Mirabella M., Ricci E., Belsito A., Abbondanza C.,
RA   Servidei S., Puca A.A., Tonali P., Puca G.A., Nigro V.;
RT   "Gamma1- and gamma2-syntrophins, two novel dystrophin-binding proteins
RT   localized in neuronal cells.";
RL   J. Biol. Chem. 275:15851-15860(2000).
CC   -!- FUNCTION: Adapter protein that binds to and probably organizes the
CC       subcellular localization of a variety of proteins. May link
CC       various receptors to the actin cytoskeleton and the dystrophin
CC       glycoprotein complex (By similarity).
CC   -!- SUBUNIT: Interacts with the dystrophin protein DMD and related
CC       proteins DTNA and DTNB.
CC   -!- SUBCELLULAR LOCATION: Membrane-associated (Probable). In skeletal
CC       muscle, it localizes at the cytoplasmic side of the sarcolemmal
CC       membrane.
CC   -!- TISSUE SPECIFICITY: Widely expressed. Strong expression in brain
CC       and testis. In CNS, it is expressed in the perikaryon and proximal
CC       portion of the neuronal processes. Strong expression in the
CC       hippocampus, neuron-rich dendate granule cells, and pyramidal cell
CC       layers. Highly expressed in neurons of the cerebral cortex. Also
CC       expressed in the cerebellar cortex, deep cerebellar nuclei,
CC       thalamus, and basal ganglia.
CC   -!- DOMAIN: The association with dystrophin or related proteins
CC       probably leaves the PDZ domain available to recruit proteins to
CC       the membrane (By similarity).
CC   -!- SIMILARITY: Belongs to the syntrophin family.
CC   -!- SIMILARITY: Contains 1 PDZ/DHR domain.
CC   -!- SIMILARITY: Contains 1 PH domain.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ003029; CAB92969.1; -.
DR   HSSP; P29476; 1QAV.
DR   Genew; HGNC:13741; SNTG2.
DR   GO; GO:0016013; C:syntrophin complex; TAS.
DR   GO; GO:0007417; P:central nervous system development; TAS.
DR   InterPro; IPR001478; PDZ.
DR   InterPro; IPR001849; PH.
DR   Pfam; PF00595; PDZ; 1.
DR   SMART; SM00228; PDZ; 1.
DR   SMART; SM00233; PH; 1.
DR   PROSITE; PS50106; PDZ; 1.
DR   PROSITE; PS50003; PH_DOMAIN; FALSE_NEG.
KW   Actin-binding; Cytoskeleton; Membrane; Multigene family.
FT   DOMAIN       73    156       PDZ.
FT   DOMAIN      296    421       PH.
FT   DOMAIN        6      9       POLY-PRO.
SQ   SEQUENCE   539 AA;  60246 MW;  0D3B1E24D2CAEF88 CRC64;

  Query Match             14.2%;  Score 79;  DB 1;  Length 539;
  Best Local Similarity   31.2%;  Pred. No. 3.7;
  Matches   30;  Conservative   12;  Mismatches   34;  Indels   20;  Gaps    4;

Qy         26 PTFQLLPQNSLETTPSSVTSESSS------------GTTTGPSASWSNSKASPYLDTRV 72
              | |  ||  |    |||  |  :|              :|| ||:  |      |  : |
Db        159 PAFLKLPLGS--PGPSSDHSSGASSPLFDSGLHLNGNSSTTAPSSPSSPIAKDPRYEKRW 216

Qy         73 ILSLDVPIGLLRILLEQARYKAARNQAATNA-QILA 107
              : :| ||: : ||    :||||   :   || ::||
Db        217 LDTLSVPLSMARI----SRYKAGTEKLRWNAFEVLA 248


RESULT 7
MUCL_RAT
ID   MUCL_RAT       STANDARD;      PRT;   837 AA.
AC   P98089;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Intestinal mucin-like protein (MLP) (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Intestine;
RX   MEDLINE=92184794; PubMed=1371999;
RA   Xu G., Huan L.-J., Khatri I., Wang D., Bennick A., Fahim R.E.F.,
RA   Forstner G.G., Forstner J.F.;
RT   "cDNA for the carboxyl-terminal region of a rat intestinal mucin-like
RT   peptide.";
RL   J. Biol. Chem. 267:5401-5407(1992).
CC   -!- SUBUNIT: Multimeric.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: COATS THE EPITHELIA OF THE INTESTINES.
CC   -!- SIMILARITY: Contains 2 VWFC domains.
CC   -!- SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M81920; -; NOT_ANNOTATED_CDS.
DR   InterPro; IPR006208; Cys_knot.
DR   InterPro; IPR006207; Cys_knot_C.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR002919; TIL_Cysrich.
DR   InterPro; IPR001007; VWF_C.
DR   InterPro; IPR001846; VWF_D.
DR   Pfam; PF00007; Cys_knot; 1.
DR   Pfam; PF00093; vwc; 1.
DR   Pfam; PF00094; vwd; 1.
DR   SMART; SM00041; CT; 1.
DR   SMART; SM00214; VWC; 2.
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DR   SMART; SM00216; VWD; 1.
DR   PROSITE; PS01185; CTCK_1; 1.
DR   PROSITE; PS01225; CTCK_2; 1.
DR   PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR   PROSITE; PS01208; VWFC_1; 2.
DR   PROSITE; PS50184; VWFC_2; 2.
KW   Repeat; Glycoprotein.
FT   NON_TER       1      1
FT   DOMAIN      149    837       PROBABLY IMPORTANT FOR DISULFIDE-BOND
FT                                MEDIATED MUCIN POLYMERIZATION (LINK
FT                                DOMAIN).
FT   DOMAIN       17     70       5 X 11 AA APPROXIMATE TANDEM REPEATS.
FT   REPEAT       17     27       1.
FT   REPEAT       28     38       2.
FT   REPEAT       39     50       3.
FT   REPEAT       51     62       4.
FT   REPEAT       63     70       5 (INCOMPLETE).
FT   DOMAIN       74    139       V (SIMILAR TO VWF A3-D4 CONJUNCTION
FT                                REGION).
FT   DOMAIN      140    517       I (SIMILAR TO VWF DOMAINS D1-D4).
FT   DOMAIN      472    543       VWFC 1.
FT   DOMAIN      581    648       VWFC 2.
FT   DOMAIN      732    817       CTCK.
FT   DISULFID    732    779       BY SIMILARITY.
FT   DISULFID    746    793       BY SIMILARITY.
FT   DISULFID    755    809       BY SIMILARITY.
FT   DISULFID    759    811       BY SIMILARITY.
FT   DISULFID      ?    816       BY SIMILARITY.
FT   CARBOHYD     91     91       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    164    164       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    278    278       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    289    289       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    344    344       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    410    410       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    444    444       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    515    515       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    538    538       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    612    612       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    627    627       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    695    695       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    727    727       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    749    749       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   837 AA;  91499 MW;  6335BCDCAC897F35 CRC64;

  Query Match             13.6%;  Score 76;  DB 1;  Length 837;
  Best Local Similarity   37.0%;  Pred. No. 12;
  Matches   17;  Conservative   11;  Mismatches   16;  Indels    2;  Gaps    1;

Qy         21 PGTPIPTFQLLPQNSLETTPSSVTSESSSGTTTGPSASWSNSKASP 66
              | || |:    | :|  ||||: :: ||  | : | :  ::||::|
Db         20 PSTPPPSTPTTPTSSQTTTPSTPSTTSSKSTPSTPQS--TSSKSTP 63


RESULT 8
N214_HUMAN
ID   N214_HUMAN     STANDARD;      PRT;  2090 AA.
AC   P35658;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Nuclear pore complex protein Nup214 (Nucleoporin Nup214) (214 kDa
DE   nucleoporin) (CAN protein).
GN   NUP214 OR CAN OR CAIN.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=92195315; PubMed=1549122;
RA   Von Lindern M., Fornerod M., Van Baal S., Jaegle M., De Wit T.,
RA   Buijs A., Grosveld G.;
RT   "The translocation (6;9), associated with a specific subtype of acute
RT   myeloid leukemia, results in the fusion of two genes, dek and can,
RT   and the expression of a chimeric, leukemia-specific dek-can mRNA.";
RL   Mol. Cell. Biol. 12:1687-1697(1992).
RN   [2]
RP   CHARACTERIZATION.
RX   MEDLINE=94151361; PubMed=8108440;
RA   Kraemer D., Wozniak R.W., Blobel G., Radu A.;
RT   "The human CAN protein, a putative oncogene product associated with
RT   myeloid leukemogenesis, is a nuclear pore complex protein that faces
RT   the cytoplasm.";
RL   Proc. Natl. Acad. Sci. U.S.A. 91:1519-1523(1994).
CC   -!- FUNCTION: May serve as a docking site in the receptor-mediated
CC       import of substrates across the nuclear pore complex.
CC   -!- SUBUNIT: Homodimer. Interacts with DDX19 and NUP88.
CC   -!- SUBCELLULAR LOCATION: Nuclear pore complex. Cytoplasmic filaments.
CC   -!- TISSUE SPECIFICITY: Expressed in thymus, spleen, bone marrow,
CC       kidney, brain and testis, but hardly in all other tissues or in
CC       whole embryos during development.
CC   -!- DOMAIN: Contains F-G repeats.
CC   -!- PTM: Probably glycosylated as it reacts with wheat germ agglutinin
CC       (WGA).
CC   -!- DISEASE: Implicated in a subset of acute myeloid leukemia (acute
CC       nonlymphocytic leukemia) (AML) carrying a chromosomal
CC       translocation t(6;9)(p23;q34) that results in the formation of a
CC       DEK-CAN fusion gene.
CC   -!- DISEASE: Involved in some cases of acute undifferentiated leukemia
CC       (AUL) through a chromosomal translocation t(6;9)(q21;q34.1) that
CC       involves NUP214/CAN and SET.
CC   -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC       WWW="http://www.infobiogen.fr/services/chromcancer/Genes/CAN.html".
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X64228; CAA45535.1; -.
DR   PIR; S26058; S26058.
DR   Genew; HGNC:8064; NUP214.
DR   MIM; 114350; -.
DR   GO; GO:0005643; C:nuclear pore; TAS.
DR   GO; GO:0005215; F:transporter activity; TAS.
DR   InterPro; IPR004325; Nucleoporin_FG.
DR   InterPro; IPR001680; WD40.
DR   Pfam; PF03093; Nucleoporin_FG; 22.
DR   SMART; SM00320; WD40; 2.
KW   Nuclear protein; Transport; Proto-oncogene; Chromosomal translocation;
KW   Repeat; Glycoprotein.
FT   DOMAIN      481   2076       11 X 5 AA APPROXIMATE REPEATS.
FT   DOMAIN     1409   2084       18 X 4 AA APPROXIMATE REPEATS.
FT   DOMAIN     1427   2085       11 X 3 AA APPROXIMATE REPEATS.
FT   DOMAIN     1213   2090       PRO/SER/THR-RICH.
FT   DOMAIN      740    768       LEUCINE-ZIPPER 1.
FT   DOMAIN      861    882       LEUCINE-ZIPPER 2.
FT   SITE        812    813       BREAKPOINT.
SQ   SEQUENCE  2090 AA;  213766 MW;  6DBE767FDD857F8F CRC64;

  Query Match             13.6%;  Score 75.5;  DB 1;  Length 2090;
  Best Local Similarity   43.1%;  Pred. No. 36;
  Matches   22;  Conservative    4;  Mismatches   20;  Indels    5;  Gaps    2;

Qy         21 PGTPIPTFQLLPQNSLETTPS-SVTSESSSGTTTGPSASWS----NSKASP 66
              |  || || |||     |  | :| || | ||   |:|    :|||:|
Db        463 PAAPIATFSLLPAGGAPTVFSFGSSSLKSSATVTGEPPSYSSGSDSSKAAP 513


RESULT 9
CRF_HUMAN
ID   CRF_HUMAN      STANDARD;      PRT;   196 AA.
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AC   P06850;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Corticoliberin precursor (Corticotropin-releasing factor) (CRF)
DE   (Corticotropin releasing hormone).
GN   CRH.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84057755; PubMed=6605851;
RA   Shibahara S., Morimoto Y., Furutani Y., Notake M., Takahashi H.,
RA   Shimizu S., Horikawa S., Numa S.;
RT   "Isolation and sequence analysis of the human corticotropin-releasing
RT   factor precursor gene.";
RL   EMBO J. 2:775-779(1983).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89137721; PubMed=2783917;
RA   Robinson B.G., D'Angio L.A. Jr., Pasieka K.B., Majzoub J.A.;
RT   "Preprocorticotropin releasing hormone: cDNA sequence and in vitro
RT   processing.";
RL   Mol. Cell. Endocrinol. 61:175-180(1989).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   STRUCTURE BY NMR OF 154-194.
RX   MEDLINE=93234434; PubMed=8386360;
RA   Romier C., Bernassau J.-M., Cambillau C., Darbon H.;
RT   "Solution structure of human corticotropin releasing factor by 1H NMR
RT   and distance geometry with restrained molecular dynamics.";
RL   Protein Eng. 6:149-156(1993).
CC   -!- FUNCTION: This hormone from hypothalamus regulates the release of
CC       corticotropin from pituitary gland.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the sauvagine/corticotropin-releasing
CC       factor/urotensin I family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; V00571; CAA23834.1; -.
DR   EMBL; BC002599; AAH02599.1; -.
DR   EMBL; BC011031; AAH11031.1; -.
DR   PIR; A30327; A30327.
DR   Genew; HGNC:2355; CRH.
DR   MIM; 122560; -.
DR   GO; GO:0005625; C:soluble fraction; TAS.
DR   GO; GO:0005184; F:neuropeptide hormone activity; TAS.
DR   GO; GO:0007611; P:learning and/or memory; TAS.
DR   GO; GO:0007567; P:parturition; TAS.
DR   GO; GO:0007565; P:pregnancy; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   GO; GO:0007268; P:synaptic transmission; TAS.
DR   InterPro; IPR000187; corticoliberin.
DR   InterPro; IPR003620; Urocortin_CRF.
DR   Pfam; PF00473; CRF; 1.
DR   PRINTS; PR01612; CRFFAMILY.
DR   ProDom; PD005970; Urocortin_CRF; 1.
DR   SMART; SM00039; CRF; 1.
DR   PROSITE; PS00511; CRF; 1.
KW   Hormone; Amidation; Hypothalamus; Cleavage on pair of basic residues;
KW   Signal.
FT   SIGNAL        1     24       PROBABLE.
FT   PROPEP       25    153
FT   PEPTIDE     154    194       CORTICOLIBERIN.
FT   MOD_RES     194    194       AMIDATION (G-195 PROVIDE AMIDE GROUP).
SQ   SEQUENCE   196 AA;  21422 MW;  0CCDFF05BE364E92 CRC64;

  Query Match             13.4%;  Score 74.5;  DB 1;  Length 196;
  Best Local Similarity   26.8%;  Pred. No. 3.3;
  Matches   22;  Conservative   19;  Mismatches   36;  Indels    5;  Gaps    2;

Qy         30 LLPQNSLETTPSSVTSESSSGTTTGPSASWSNSKASPYLDTRVILSLDVPIGLLRILLEQ 89
              |||: ||: :|:::    :    |   :   : |        :|||:   ||| :||
Db        120 LLPRRSLD-SPAALAERGARNALGGHQEAPERERRS----EEPPISLDLTFHLLREVLEM 174

Qy         90 ARYKAARNQAATNAQILAHVGR 111
              || :    || :| :::  :|:
Db        175 ARAEQLAQQAHSNRKLMEIIGK 196


RESULT 10
VV_SV5
ID   VV_SV5         STANDARD;      PRT;   222 AA.
AC   P11207;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-JUL-1989 (Rel. 11, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Nonstructural protein V.
GN   P/V.
OS   Simian virus 5 (strain W3) (SV5).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX   NCBI_TaxID=11208;
RN   [1]
RP   SEQUENCE FROM N.A., AND RNA EDITING.
RX   MEDLINE=88311091; PubMed=3044614;
RA   Thomas S.M., Lamb R.A., Paterson R.G.;
RT   "Two mRNAs that differ by two nontemplated nucleotides encode the
RT   amino coterminal proteins P and V of the paramyxovirus SV5.";
RL   Cell 54:891-902(1988).
CC   -!- RNA EDITING: Modified_positions=164; Note=Partially edited. RNA
CC       editing at this position consists of an insertion of two guanine
CC       nucleotides. The sequence displayed here is the V protein, derived
CC       from the unedited RNA. The edited RNA gives rise to the P protein
CC       (AC P11208).
CC   -!- SIMILARITY: TO THE V PROTEIN OF OTHER PARAMYXOVIRUSES.
CC   ---------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; J03142; AAA47882.1; -.
DR   EMBL; AF052755; AAC95512.1; -.
DR   PIR; A31594; MNNZSP.
DR   InterPro; IPR004897; Paramyx_P_V.
DR   Pfam; PF03210; Paramyx_P_V; 1.
KW   Nonstructural protein; RNA editing.
FT   DOMAIN      190    218       CYS-RICH.
SQ   SEQUENCE   222 AA;  23935 MW;  13D2F1627D15AFA3 CRC64;

  Query Match             12.8%;  Score 71.5;  DB 1;  Length 222;
  Best Local Similarity   32.3%;  Pred. No. 7.3;
  Matches   31;  Conservative    9;  Mismatches   29;  Indels   27;  Gaps    5;

Qy         20 VPGTPIPTFQLLPQNSLETTPSSVTSESSSGTTTGPSASWSNSKASPY----LDTRVILS 75
              ||| |||     |   |::|||: |    || |  || |:   | : :    | || |
Db         93 VPGKPIPN----PLLGLDSTPSTQTVLDLSGKTL-PSGSYKGVKLAKFGKENLMTRFI-- 145

Qy         76 LDVPIGLLRILLEQARYKAARNQAATNAQILAHVGR 111
                        |: |     |  ||:: |    ||
Db        146 -----------EEPR----ENPIATSSPIDFKRGR 165


RESULT 11
GCM1_MOUSE
ID   GCM1_MOUSE     STANDARD;      PRT;   436 AA.
AC   P70348; O09103;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Chorion-specific transcription factor GCMa (Glial cells missing
DE   homolog 1) (GCM motif protein 1) (mGCMa) (mGCM1).
GN   GCM1 OR GCMA.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=96409308; PubMed=8814290;
RA   Altshuller Y., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA   Frohman M.A.;
RT   "Gcm1, a mammalian homolog of Drosophila glial cells missing.";
RL   FEBS Lett. 393:201-204(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=97121489; PubMed=8962155;
RA   Akiyama Y., Hosoya T., Poole A.M., Hotta Y.;
RT   "The gcm-motif: a novel DNA binding motif conserved in Drosophila and
RT   mammals.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:14912-14916(1996).
CC   -!- FUNCTION: Transcription factor that is necessary for placental
CC       development (By similarity).
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- TISSUE SPECIFICITY: Placenta specific.
CC   -!- SIMILARITY: Contains 1 GCM domain.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; U59876; AAC52822.1; -.
DR   EMBL; D88612; BAA13650.1; -.
DR   PIR; S74257; S74257.
DR   TRANSFAC; T02307; -.
DR   MGD; MGI:108045; Gcm1.
DR   GO; GO:0003677; F:DNA binding; IDA.
DR   GO; GO:0008270; F:zinc ion binding; IDA.
DR   InterPro; IPR003902; GCM_motif.
DR   Pfam; PF03615; GCM; 1.
DR   PROSITE; PS50807; GCM; 1.
KW   Transcription regulation; DNA-binding; Nuclear protein;
KW   Developmental protein.
FT   DOMAIN       14    169       GCM.
FT   CONFLICT    211    211       G -> S (IN REF. 2).
FT   CONFLICT    230    230       N -> K (IN REF. 2).
FT   CONFLICT    241    241       S -> N (IN REF. 2).
FT   CONFLICT    413    413       D -> E (IN REF. 2).
SQ   SEQUENCE   436 AA;  49589 MW;  99F4E441800582DB CRC64;

  Query Match             12.8%;  Score 71.5;  DB 1;  Length 436;
  Best Local Similarity   35.3%;  Pred. No. 15;
  Matches   24;  Conservative    6;  Mismatches   31;  Indels    7;  Gaps    4;

Qy         18 LFVPGTPIPT----FQLLP-QNSLETTPSSVTSESSSGTTTGPSASWSNSKASPYLD-TR 71
              :: |  |:|     :   | |||||  |  | ||  :    |    |||    || :
Db        311 IYYPAYPLPVASWPYDYFPSQNSLEHLPQQVPSEPPA-AQPGCHPLWSNPGGEPYEEKVS 369

Qy         72 VILSLDVP 79
              | ||  ||
Db        370 VDLSSYVP 377


RESULT 12
AB31_ARATH
ID   AB31_ARATH     STANDARD;      PRT;   519 AA.
AC   Q9FYL3;
DT   15-MAR-2004 (Rel. 43, Created)
DT   15-MAR-2004 (Rel. 43, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Inner membrane ALBINO3-like protein 1, chloroplast precursor (Ath4).
GN   ALB3L1 OR AT1G24490 OR F21J9.16.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia;
RX   MEDLINE=21016719; PubMed=11130712;
RA   Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA   White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA   Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA   Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA   Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA   Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA   Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA   Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA   Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA   Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA   Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA   Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA   Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA   Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA   Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA   Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT   "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT   thaliana.";
RL   Nature 408:816-820(2000).
CC   -!- FUNCTION: Probably required for the insertion of integral membrane
CC       proteins into the chloroplast thylakoid membrane (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Chloroplast
CC       thylakoid membrane (Potential).
CC   -!- SIMILARITY: Belongs to the OXA1/oxaA family.
CC   ----------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; AC000103; AAF97961.1; -.
DR   PIR; H86378; H86378.
DR   InterPro; IPR001708; 60kDa_innermeb.
DR   Pfam; PF02096; 60KD_IMP; 1.
KW   Chloroplast; Membrane; Inner membrane; Transit peptide; Transmembrane.
FT   TRANSIT       1      ?       CHLOROPLAST (POTENTIAL).
FT   CHAIN         ?    519       INNER MEMBRANE ALBINO3-LIKE PROTEIN 1.
FT   TRANSMEM    115    135       POTENTIAL.
FT   TRANSMEM    147    167       POTENTIAL.
FT   TRANSMEM    204    224       POTENTIAL.
FT   TRANSMEM    283    303       POTENTIAL.
FT   TRANSMEM    322    342       POTENTIAL.
SQ   SEQUENCE   519 AA;  57507 MW;  A4CE0A5EBF2CB769 CRC64;

  Query Match             12.8%;  Score 71.5;  DB 1;  Length 519;
  Best Local Similarity   31.3%;  Pred. No. 19;
  Matches   26;  Conservative   11;  Mismatches   31;  Indels   15;  Gaps    3;

Qy         41 SSVTSESSSGTTTGPSAS--WSNSKASPYLDT-----------RVILSLDVPIGLLRIL 86
              || | || :|||| : | | : |: |::|              | |    | || :|
Db         76 SSETFESVAGTTTKTTQSNDWFSGIAN-YMETILKVLKDGLSTVHVPYSYGFAIILLTVL 134

Qy         87 LEQARYKAARNQAATNAQILAHV 109
              :: | :  : | |  |  | ||
Db        135 VKAATFPLTKKQVFTMISFLVHV 157


RESULT 13
VMT1_RAT
ID   VMT1_RAT       STANDARD;      PRT;   521 AA.
AC   Q01818;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Chromaffin granule amine transporter (Vesicular amine transporter 1)
DE   (VAT1) (Solute carrier family 18 member 1).
GN   SLC18A1 OR VMAT1 OR CGAT.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92370677; PubMed=1505023;
RA   Liu Y., Peter D., Roghani A., Schuldiner S., Prive G.G.,
RA   Eisenberg D., Brecha N., Edwards R.H.;
RT   "A cDNA that suppresses MPP+ toxicity encodes a vesicular amine
RT   transporter.";
RL   Cell 70:539-551(1992).
CC   -!- FUNCTION: Involved in the vesicular transport of biogenic amines.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Vesicular
CC       membrane.
CC   -!- TISSUE SPECIFICITY: Adrenal gland.
CC   -!- SIMILARITY: Belongs to the major facilitator (MFS) superfamily.
CC       Vesicular transporter family.
CC   ---------------------------------------------------------------------------
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CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
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CC   ---------------------------------------------------------------------------
DR   EMBL; M97380; AAA40921.1; -.
DR   PIR; A43319; A43319.
DR   InterPro; IPR007114; MFS.
DR   InterPro; IPR005828; Sub_transporter.
DR   Pfam; PF00083; sugar_tr; 1.
DR   PROSITE; PS50850; MFS; 1.
KW   Transport; Transmembrane; Glycoprotein; Neurotransmitter transport.
FT   DOMAIN        1     21       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     22     42       POTENTIAL.
FT   DOMAIN       43    135       VESICULAR LUMEN (POTENTIAL).
FT   TRANSMEM    136    155       POTENTIAL.
FT   DOMAIN      156    164       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    165    185       POTENTIAL.
FT   DOMAIN      186    194       VESICULAR LUMEN (POTENTIAL).
FT   TRANSMEM    195    215       POTENTIAL.
FT   DOMAIN      216    224       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    225    247       POTENTIAL.
FT   DOMAIN      248    253       VESICULAR LUMEN (POTENTIAL).
FT   TRANSMEM    254    276       POTENTIAL.
FT   DOMAIN      277    296       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    297    316       POTENTIAL.
FT   DOMAIN      317    332       VESICULAR LUMEN (POTENTIAL).
FT   TRANSMEM    333    357       POTENTIAL.
FT   DOMAIN      358    362       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    363    383       POTENTIAL.
FT   DOMAIN      384    394       VESICULAR LUMEN (POTENTIAL).
FT   TRANSMEM    395    415       POTENTIAL.
FT   DOMAIN      416    419       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    420    440       POTENTIAL.
FT   DOMAIN      441    445       VESICULAR LUMEN (POTENTIAL).
FT   TRANSMEM    446    467       POTENTIAL.
FT   DOMAIN      468    521       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     58     58       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     87     87       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    104    104       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   521 AA;  55935 MW;  DCDC0D0AF0EC15D4 CRC64;

  Query Match             12.8%;  Score 71.5;  DB 1;  Length 521;
  Best Local Similarity   33.3%;  Pred. No. 19;
  Matches   22;  Conservative    8;  Mismatches   25;  Indels   11;  Gaps    2;

Qy          6 LVVFVVLMLDRILFVPGTPI-PTFQLLPQNSLETTPSSVTSESSSGTTTGPSASWSNSKA 64
              :|||| |:|| :|     || |||          ::   :|:|    ||| |   :
Db         25 VVVFVALLLDNMLLTVVVPIVPTFLY----------ATEFKDSNSSLHRGPSVSSQQALT 74

Qy         65 SPYLDT 70
              ||   |
Db         75 SPAFST 80


RESULT 14
AMYH_YEAST
ID   AMYH_YEAST     STANDARD;      PRT;  1367 AA.
AC   P08640; P08068;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Glucoamylase S1/S2 precursor (EC 3.2.1.3) (Glucan 1,4-alpha-
DE   glucosidase) (1,4-alpha-D-glucan glucohydrolase).
GN   STA1 OR STA2 OR MAL5 OR YIR019C.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288c / AB972;
RX   MEDLINE=97313266; PubMed=9169870;
RA   Churcher C.M., Bowman S., Badcock K., Bankier A., Brown D.,
RA   Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N.,
RA   Harris D.E., Horsnell T., Hunt S., Jagels K., Jones M., Lye G.,
RA   Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley N.,
RA   Skelton J., Smith V., Walsh S., Whitehead S., Barrell B.G.;
RT   "The nucleotide sequence of Saccharomyces cerevisiae chromosome IX.";
RL   Nature 387:84-87(1997).
RN   [2]
RP   SEQUENCE OF 1-242 AND 762-1331 FROM N.A.
RX   MEDLINE=87194600; PubMed=3106330;
```

```
RA   Yamashita I., Nakamura M., Fukui S.;
RT   "Gene fusion is a possible mechanism underlying the evolution of
RT   STA1.";
RL   J. Bacteriol. 169:2142-2149(1987).
RN   [3]
RP   SEQUENCE OF 1-31 FROM N.A.
RC   STRAIN=SPX101-1C;
RX   MEDLINE=89031230; PubMed=3141213;
RA   Pardo J.M., Ianez E., Zalacain M., Claros M.G., Jimenez A.;
RT   "Similar short elements in the 5' regions of the STA2 and SGA genes
RT   from Saccharomyces cerevisiae.";
RL   FEBS Lett. 239:179-184(1988).
CC   -!- CATALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-
CC       glucose residues successively from non-reducing ends of the chains
CC       with release of beta-D-glucose.
CC   -!- SIMILARITY: TO S.POMBE SPBC215.13.
CC   -!- SIMILARITY: SOME, TO S.POMBE SPCC285.13C.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; Z38061; CAA86176.1; -.
DR   EMBL; M16164; AAA35014.1; -.
DR   EMBL; M16165; AAA35015.1; -.
DR   EMBL; X13857; CAA32069.1; -.
DR   PIR; S48478; S48478.
DR   GermOnline; 139731; -.
DR   SGD; S0001458; MUC1.
DR   GO; GO:0005886; C:plasma membrane; IDA.
DR   GO; GO:0030447; P:filamentous growth; IDA.
DR   GO; GO:0007125; P:invasive growth; IMP.
DR   GO; GO:0007124; P:pseudohyphal growth; IMP.
KW   Hydrolase; Glycosidase; Polysaccharide degradation; Glycoprotein;
KW   Signal; Multigene family.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22   1367       GLUCOAMYLASE S1/S2.
FT   DOMAIN      210   1367       SER/THR-RICH.
FT   CARBOHYD    817    817       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    874    874       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   1367 AA;  136110 MW;  91C00E2DBD61AA9D CRC64;

  Query Match             12.7%;  Score 71;  DB 1;  Length 1367;
  Best Local Similarity   38.6%;  Pred. No. 61;
  Matches   17;  Conservative    6;  Mismatches    9;  Indels   12;  Gaps    1;

Qy         23 TPIPTFQLLPQNSLETTPSSVTSESSSGTTTGPSASWSNSKASP 66
              ||:|           |||| |:|||| ||:| : | ::|
Db        312 TPVP-----------TPSSSTTESSSAPVPTPSSSTTESSSAP 343


RESULT 15
RRPP_SV5
ID   RRPP_SV5       STANDARD;      PRT;   392 AA.
AC   P11208;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-JUL-1989 (Rel. 11, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   RNA polymerase alpha subunit (EC 2.7.7.48) (P protein).
GN   P/V.
OS   Simian virus 5 (strain W3) (SV5).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX   NCBI_TaxID=11208;
RN   [1]
RP   SEQUENCE FROM N.A., AND RNA EDITING.
RX   MEDLINE=88311091; PubMed=3044614;
RA   Thomas S.M., Lamb R.A., Paterson R.G.;
RT   "Two mRNAs that differ by two nontemplated nucleotides encode the
RT   amino coterminal proteins P and V of the paramyxovirus SV5.";
RL   Cell 54:891-902(1988).
CC   -!- FUNCTION: Essential component of the RNA polymerase and the
CC       nascent chain assembly complex. Also required during RNA
CC       synthesis.
CC   -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC       {RNA}(N).
CC   -!- RNA EDITING: Modified_positions=164; Note=Partially edited. RNA
CC       editing at this position consists of an insertion of two guanine
CC       nucleotides. The sequence displayed here is the P protein, derived
CC       from the edited RNA. The unedited RNA version gives rise to the V
CC       protein (AC P11207).
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J03142; -; NOT_ANNOTATED_CDS.
DR   EMBL; AF052755; AAC95513.1; -.
DR   PIR; B31594; RRNZSP.
DR   InterPro; IPR004897; Paramyx_P_V.
DR   Pfam; PF03210; Paramyx_P_V; 1.
KW   Transferase; RNA-directed RNA polymerase; Nucleocapsid;
KW   Phosphorylation; RNA editing.
SQ   SEQUENCE   392 AA;  42106 MW;  A95D21FD125E8559 CRC64;

  Query Match             12.7%;  Score 70.5;  DB 1;  Length 392;
  Best Local Similarity   39.7%;  Pred. No. 17;
  Matches   23;  Conservative    6;  Mismatches   20;  Indels    9;  Gaps    3;

Qy         20 VPGTPIPTFQLLPQNSLETTPSSVTSESSSGTTTGPSASWSNSKASPY----LDTRVI 73
              ||| |||     |   |::|||: |    || |  || |:   | : :    | || |
Db         93 VPGKPIPN----PLLGLDSTPSTQTVLDLSGKTL-PSGSYKGVKLAKFGKENLMTRFI 145


Search completed: April 20, 2004, 18:55:21
Job time : 20.9333 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 20, 2004, 18:52:07 ; Search time 20.16 Seconds
(without alignments)
534.397 Million cell updates/sec

Title: US-09-919-473-10
Perfect score: 557
Sequence: 1 MTRWALVVFVVLMLDRILFV.....KAARNQAATNAQILAHVGRR 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	79	14.2	338	2	T39159	hypothetical prote
2	77.5	13.9	889	2	AB0790	probable two-compo
3	76	13.6	837	2	A42112	mucin-like peptide
4	75.5	13.6	2090	2	S26058	probable transform
5	74.5	13.4	196	2	A30327	corticoliberin pre
6	74	13.3	2578	2	A56922	transcription fact
7	73.5	13.2	164	2	I53641	mucin 5AC - human
8	73	13.1	125	2	D72475	hypothetical prote
9	73	13.1	802	2	G87578	TonB-dependent rec
10	72.5	13.0	486	2	B55886	dopamine receptor
11	72.5	13.0	526	2	T14875	hypothetical prote
12	72.5	13.0	3283	2	AC1018	large repetitive p
13	72	12.9	431	2	T38260	hypothetical prote
14	71.5	12.8	222	1	MNNZSP	nonstructural prot
15	71.5	12.8	276	2	T29689	hypothetical prote
16	71.5	12.8	436	2	S74257	glial cells missin
17	71.5	12.8	519	2	H86378	protein F21J9.16 [
18	71.5	12.8	521	2	A43319	chromaffin granule
19	71.5	12.8	2529	2	A56923	transcription fact
20	71	12.7	476	2	T23728	hypothetical prote
21	71	12.7	1367	1	S48478	glucan 1,4-alpha-g
22	71	12.7	1796	2	AC1895	serine/threonine k
23	70.5	12.7	392	1	RRNZSP	polymerase-associa
24	70.5	12.7	1036	2	B83466	probable RND efflu
25	70.5	12.7	4377	2	A55575	ankyrin 3, long sp
26	70	12.6	247	2	H71565	hypothetical prote
27	70	12.6	292	2	I51171	transcription fact
28	70	12.6	402	2	G90254	conserved hypothet
29	70	12.6	500	1	JC2231	prostaglandin-I sy
30	69.5	12.5	187	1	RHRTCE	corticoliberin pre
31	69.5	12.5	322	2	F84616	probable bHLH tran
32	69.5	12.5	636	2	S63131	probable membrane
33	69.5	12.5	1324	2	S52863	DNA-binding protei
34	69	12.4	549	2	S32987	hypothetical prote
35	69	12.4	682	2	T47473	receptor-like prot
36	69	12.4	808	2	T23129	hypothetical prote
37	69	12.4	1151	2	T18535	high molecular mas
38	68.5	12.3	532	2	I38658	vesicular acetylch
39	68	12.2	122	2	S60262	corticotensin - ra
40	68	12.2	145	1	UOCA1	urotensin I precur
41	68	12.2	162	2	A31343	corticoliberin 1 p
42	68	12.2	254	2	D88560	protein F58A4.1 [i
43	68	12.2	303	2	S40973	hypothetical prote
44	68	12.2	469	1	P2WLPR	L2 protein - human
45	68	12.2	580	2	T37664	hypothetical prote

ALIGNMENTS

RESULT 1
T39159
hypothetical protein SPAC8E11.05c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Mar-2000
C;Accession: T39159
R;McLean, J.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, February 1998
A;Reference number: Z21831
A;Accession: T39159
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-338 <MCL>
A;Cross-references: EMBL:AL021817; PIDN:CAA17026.1; GSPDB:GN00066; SPDB:SPAC8E11.05c
A;Experimental source: strain 972h-; cosmid c8E11
C;Genetics:
A;Gene: SPDB:SPAC8E11.05c
A;Map position: 1
C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC8E11.05c

Query Match 14.2%; Score 79; DB 2; Length 338;
Best Local Similarity 27.7%; Pred. No. 2.6;
Matches 28; Conservative 9; Mismatches 28; Indels 36; Gaps 3;

```
Qy          8 VFVVLMLDRILFVPGTPIPTFQLLPQNSLETTPSSVTSESSSGTTTGPSASWSNSKASPY 67
              :|:| |         | |:   :|||       |||:  | :|| |    |  :   |:  ||
Db        202 IFLVTM--------GLPVDLDELLP------TPSTQGSFNSSRTIELSSVTLPKSEDEPY 247

Qy         68 LDTRVILSLDVPIGLLRILLEQARYKAARNQAATNAQILAH 108
              ||                    | |||   : |   | |
Db        248 LD---------------------YSAARRLCSINKDALTH 266
```

RESULT 2
AB0790
probable two-component system sensor kinase STY2494 [imported] - Salmonella enterica subs
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AB0790
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AB0790
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-889 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD07500.1; PID:g16503495; GSPDB:GN00176

```
C;Genetics:
A;Gene: STY2494

  Query Match             13.9%;  Score 77.5;  DB 2;  Length 889;
  Best Local Similarity   26.4%;  Pred. No. 12;
  Matches   33;  Conservative   18;  Mismatches   39;  Indels   35;  Gaps    5;

Qy         18 LFVPGTPIPTFQLLP-------QNSLETTPSSVTSE--------SSSGTTTGPSASWSNS 62
              |  || |: :|:: |        ::| :  | |||          ||:  :||    |
Db        238 LIPPGMPLDSFRIEPDATQTTGRSSEKEAPDSVTISFNGSKIEISSALNSTGMRLIWQVP 297

Qy         63 KASPYLDT--RVILSLDVPIGLLRILL--------------EQARYKAARNQ----AATN 102
                :  |||   ::| | : |||| : |              |     || |:     | |
Db        298 FGTLLLDTLQNILLPLLLNIGLLALALFGYATFRHQPGRSTESTSGNAANNELRVLRAIN 357

Qy        103 AQILA 107
                :|::
Db        358 EEIVS 362


RESULT 3
A42112
mucin-like peptide MLP 2677 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 10-Oct-1997
C;Accession: A42112
R;Xu, G.; Huan, L.J.; Khatri, I.A.; Wang, D.; Bennick, A.; Fahim, R.E.; Forstner, G.G.;
J. Biol. Chem. 267, 5401-5407, 1992
A;Title: cDNA for the carboxyl-terminal region of a rat intestinal mucin-like peptide.
A;Reference number: A42112; MUID:92184794; PMID:1371999
A;Accession: A42112
A;Status: preliminary
A;Molecule type: nucleic acid; protein
A;Residues: 1-837 <XU1>
A;Experimental source: intestine
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIP:87420)
C;Superfamily: von Willebrand factor type C repeat homology
F;582-650/Domain: von Willebrand factor type C repeat homology <VWC>

  Query Match             13.6%;  Score 76;  DB 2;  Length 837;
  Best Local Similarity   37.0%;  Pred. No. 16;
  Matches   17;  Conservative   11;  Mismatches   16;  Indels    2;  Gaps    1;

Qy         21 PGTPIPTFQLLPQNSLETTPSSVTSESSSGTTTGPSASWSNSKASP 66
              | || |:    | :|  ||||: :: ||  | : :| :  ::||::|
Db         20 PSTPPPSTPTTPTSSQTTTPSTPSTTSSKSTPSTPQS--TSSKSTP 63


RESULT 4
S26058
probable transforming protein (can) - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
C;Accession: S26058
R;von Lindern, M.; Fornerod, M.; van Baal, S.; Jaegle, M.; de Wit, T.; Buijs, A.; Grosve
Mol. Cell. Biol. 12, 1687-1697, 1992
A;Title: The translocation (6;9), associated with a specific subtype of acute myeloid le
k-can mRNA.
A;Reference number: S26058; MUID:92195315; PMID:1549122
A;Accession: S26058
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2090 <VON>
A;Cross-references: EMBL:X64228; NID:g29652; PIDN:CAA45535.1; PID:g29653

  Query Match             13.6%;  Score 75.5;  DB 2;  Length 2090;
  Best Local Similarity   43.1%;  Pred. No. 52;
  Matches   22;  Conservative    4;  Mismatches   20;  Indels    5;  Gaps    2;

Qy         21 PGTPIPTFQLLPQNSLETTPS-SVTSESSSGTTTGPSASWS----NSKASP 66
              |  || || |||      |  |   :|  || | ||   |:|    :|||:|
Db        463 PAAPIATFSLLPAGGAPTVFSFGSSSLKSSATVTGEPPSYSSGSDSSKAAP 513


RESULT 5
A30327
corticoliberin precursor - human
N;Alternate names: corticotropin-releasing factor
N;Contains: corticoliberin
C;Species: Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Jul-1999
C;Accession: A30327; A60860; I38106
R;Robinson, B.G.; D'Angio Jr., L.A.; Pasieka, K.B.; Majzoub, J.A.
Mol. Cell. Endocrinol. 61, 175-180, 1989
A;Title: Preprocorticotropin releasing hormone: cDNA sequence and in vitro processing.
A;Reference number: A30327; MUID:89137721; PMID:2783917
A;Accession: A30327
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-196 <ROB>
R;Sasaki, A.; Tempst, P.; Liotta, A.S.; Margioris, A.N.; Hood, L.E.; Kent, S.B.H.; Sato,
J. Clin. Endocrinol. Metab. 67, 768-773, 1988
A;Title: Isolation and characterization of a corticotropin-releasing hormone-like peptide
A;Reference number: A60860; MUID:88331316; PMID:3262120
A;Accession: A60860
A;Molecule type: protein
A;Residues: 154-168,'X',170-186 <SAS>
R;Shibahara, S.; Morimoto, Y.; Furutani, Y.; Notake, M.; Takahashi, H.; Shimizu, S.; Hori
EMBO J. 2, 775-779, 1983
A;Title: Isolation and sequence analysis of the human corticotropin-releasing factor prec
A;Reference number: I38106; MUID:84057755; PMID:6605851
A;Accession: I38106
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-196 <RES>
A;Cross-references: EMBL:V00571; NID:g35355; PIDN:CAA23834.1; PID:g35356
C;Genetics:
A;Gene: GDB:CRH
A;Cross-references: GDB:119804; OMIM:122560
A;Map position: 8q13-8q13
C;Superfamily: corticoliberin-endorpholiberin; diuretic hormone homology
C;Keywords: amidated carboxyl end; hormone; hypothalamus; placenta
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-196/Product: procorticoliberin #status predicted <MAT>
F;154-194/Product: corticoliberin #status predicted <CLN>
F;154-193/Domain: diuretic hormone homology <DHH>
F;194/Modified site: amidated carboxyl end (Ile) (amide in mature form from following gly

  Query Match             13.4%;  Score 74.5;  DB 2;  Length 196;
  Best Local Similarity   26.8%;  Pred. No. 3.9;
  Matches   22;  Conservative   19;  Mismatches   36;  Indels    5;  Gaps    2;

Qy         30 LLPQNSLETTPSSVTSESSSGTTTGPSASWSNSKASPYLDTRVILSLDVPIGLLRILLEQ 89
              |||: ||: :|:::    :     |   :    : |        :|||:   ||| :||
Db        120 LLPRRSLD-SPAALAERGARNALGGHQEAPERERRS----EEPPISLDLTFHLLREVLEM 174

Qy         90 ARYKAARNQAATNAQILAHVGR 111
              || :    || :| :::  :|:
Db        175 ARAEQLAQQAHSNRKLMEIIGK 196


RESULT 6
A56922
transcription factor shn - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 17-Mar-1999
C;Accession: A56922
R;Arora, K.; Dai, H.; Kazuko, S.G.; Jamal, J.; O'Connor, M.B.; Letsou, A.; Warrior, R.
Cell 81, 781-790, 1995
A;Title: The Drosophila schnurri gene acts in the Dpp/TGFbeta signaling pathway and encod
A;Reference number: A56922; MUID:95292345; PMID:7774017
A;Accession: A56922
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tran
A;Molecule type: mRNA
A;Residues: 1-2578 <ARO>
```

```
C;Genetics:
A;Gene: FlyBase:shn
A;Cross-references: FlyBase:FBgn0003396

  Query Match             13.3%;  Score 74;  DB 2;  Length 2578;
  Best Local Similarity   30.6%;  Pred. No. 94;
  Matches   26;  Conservative   15;  Mismatches   36;  Indels    8;  Gaps    2;

Qy         24 PIPTFQLLPQNSLET-----TPSSVTSESSSGTTTGPSASWSNSKASPYLDTRVILSLDV 78
              | ||    :| :|| |      ||:: |: :||   |  | |  :||     |      |:: :
Db       1042 PKPTLVTVPVSSLSTSSLAPTPTTSTNPTSSSKTAPPPAQVNNSIIKNLLLNARGLAVRL 1101

Qy         79 PIGL---LRILLEQARYKAARNQAA 100
                :   :|:|  ||      |::||
Db       1102 AKAMMLFIRVLSVQANSAVRRSEAA 1126


RESULT 7
I53641
mucin 5AC - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Apr-2000
C;Accession: I53641
R;Ho, S.B.; Roberton, A.M.; Shekels, L.L.; Lyftogt, C.T.; Niehans, G.A.; Toribara, N.W.
Gastroenterology 109, 735-747, 1995
A;Title: Expression cloning of gastric mucin complementary DNA and localization of mucin
A;Reference number: I53641; MUID:95385930; PMID:7657101
A;Accession: I53641
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-164 <RES>
A;Cross-references: GB:L46721; NID:g945218; PIDN:AAC41774.1; PID:g945219
C;Genetics:
A;Gene: GDB:MUC5AC
A;Cross-references: GDB:454136; OMIM:158373
A;Map position: 11p15.5-11p15.5

  Query Match             13.2%;  Score 73.5;  DB 2;  Length 164;
  Best Local Similarity   34.0%;  Pred. No. 3.9;
  Matches   18;  Conservative   10;  Mismatches   22;  Indels    3;  Gaps    1;

Qy         21 PGT---PIPTFQLLPQNSLETTPSSVTSESSSGTTTGPSASWSNSKASPYLDT 70
              |||   |:||       :  || :  || :|: ||: |||  :::  :|   |
Db         35 PGTTPSPVPTTSTTSAPTTSTTSAPTTSTTSAPTTSTPSAPTTSTTLAPTTST 87


RESULT 8
D72475
hypothetical protein APE2445 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
C;Accession: D72475
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: D72475
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-125 <KAW>
A;Cross-references: DDBJ:AP000064; NID:g5105945; PIDN:BAA81460.1; PID:d1045246; PID:g510
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE2445
C;Superfamily: Aeropyrum pernix hypothetical protein APE2445

  Query Match             13.1%;  Score 73;  DB 2;  Length 125;
  Best Local Similarity   28.9%;  Pred. No. 3.2;
  Matches   26;  Conservative   10;  Mismatches   40;  Indels   14;  Gaps    2;

Qy         24 PIPTFQLLPQNS---------LETTPSSVTSESSSGTTTGPSASWSNSKASPYLDTRVIL 74
              |: |  |    |         |  |||| |  ||| |    ||:      || : | : |

Db         12 PLSTIPLTASQSSAEALCSPRLMKTPSSSTKGSSSATLPRESAT-----LSPGVSTALRL 66

Qy         75 SLDVPIGLLRILLEQARYKAARNQAATNAQ 104
                 |  :|  :      | | :  :|:|:
Db         67 QTSTPFSAVRRSIASLALKTASSMLSTSAE 96


RESULT 9
G87578
TonB-dependent receptor [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: G87578
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.F
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolona
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: G87578
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-802 <STO>
A;Cross-references: GB:AE005673; NID:g13424241; PIDN:AAK24627.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC2660

  Query Match             13.1%;  Score 73;  DB 2;  Length 802;
  Best Local Similarity   23.1%;  Pred. No. 29;
  Matches   21;  Conservative   10;  Mismatches   40;  Indels   20;  Gaps    1;

Qy         35 SLETTPSSVTSESSSGTTTGPSASWSNSKASPYLDTRVILSLDVPIGLLRILL------- 87
              |   ||: :           |     | |   | :  | | :: |: || | ::|
Db        448 SFGATPTDIIDSPFDDEPGGVGLKWENDNRSTWKQTGVFVTSDIDIGRLNLILGGRWDRY 507

Qy         88 ------------EQARYKAARNQAATNAQI 105
                         |  | ||:|  || :
Db        508 SVESQDTGFLSYTVTGRKTADRNKATWNASL 538


RESULT 10
B55886
dopamine receptor D1B - chicken
C;Species: Gallus gallus (chicken)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 17-Mar-1999
C;Accession: B55886
R;Demchyshyn, L.L.; Sugamori, K.S.; Lee, F.J.S.; Hamadanizadeh, S.A.; Niznik, H.B.
J. Biol. Chem. 270, 4005-4012, 1995
A;Title: The dopamine D1D receptor. Cloning and characterization of three pharmacological
A;Reference number: A55886; MUID:95181368; PMID:7876148
A;Accession: B55886
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tran
A;Molecule type: DNA
A;Residues: 1-486 <DEM>
A;Cross-references: GB:L36878
C;Superfamily: vertebrate rhodopsin
C;Keywords: neurotransmitter receptor

  Query Match             13.0%;  Score 72.5;  DB 2;  Length 486;
  Best Local Similarity   31.1%;  Pred. No. 18;
  Matches   23;  Conservative   13;  Mismatches   29;  Indels    9;  Gaps    2;

Qy         39 TPSSVTSESSSGTTTGPSASWSNSKASPYLDTRVILSLDVPIGLL--------RILLEQA 90
              ||| ||  |: |  ||| |  :|    |  :  ::| :|: ::         ||   |
Db        216 TPSEGTS-GSNNTVPGPSESCDSSLNRTYAISSSLISFYIPVAIMIVTYTRIYRIAQVQI 274

Qy         91 RYKAARNQAATNAQ 104
              |  ::  :|| :||
Db        275 RRISSLERAAEHAQ 288


RESULT 11
T14875
```

hypothetical protein - Salmonella typhimurium
C;Species: Salmonella typhimurium
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T14875
R;Wong, K.K.; McClelland, M.; Stillwell, L.C.; Sisk, E.C.; Thurston, S.J.; Saffer, J.D.
Infect. Immun. 66, 3365-3371, 1998
A;Title: Identification and sequence analysis of a 27-kilobase chromosomal fragment cont
ovar typhimurium LT2.
A;Reference number: Z18249; MUID:98298059; PMID:9632606
A;Accession: T14875
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-526 <WON>
A;Cross-references: EMBL:AF060869; NID:g3323584; PID:g3323592; PIDN:AAC26644.1
C;Genetics:
A;Gene: spi4_F
A;Map position: 92 min

  Query Match 13.0%; Score 72.5; DB 2; Length 526;
  Best Local Similarity 29.2%; Pred. No. 20;
  Matches 21; Conservative 14; Mismatches 22; Indels 15; Gaps 3;

```
Qy          10 VVLMLDRILFVPGTPIPTFQLLPQNSLETTPSSVTSESSSGTTTGPS---ASWSNSKASP 66
               :|: :| :     |  |||:| |:       |||:       |  ||    :  |:|
Db         162 LVITIDSV-----TDKPTFELSPE-------SSVSGHKGLTPTLTPSIVGTAEENAKVDI 209

Qy          67 YLDTRVILSLDV 78
               |:| ::: |:||
Db         210 YVDNKLVASVDV 221
```

RESULT 12
AC1018
large repetitive protein [imported] - Salmonella enterica subsp. enterica serovar Typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AC1018
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AC1018
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-3283 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD09244.1; PID:g16505248; GSPDB:GN00176
C;Genetics:
A;Gene: STY4458

  Query Match 13.0%; Score 72.5; DB 2; Length 3283;
  Best Local Similarity 29.2%; Pred. No. 1.8e+02;
  Matches 21; Conservative 14; Mismatches 22; Indels 15; Gaps 3;

```
Qy          10 VVLMLDRILFVPGTPIPTFQLLPQNSLETTPSSVTSESSSGTTTGPS---ASWSNSKASP 66
               :|: :| :     |  |||:| |:       |||:       |  ||    :  |:|
Db         326 LVITIDSV-----TDKPTFELSPE-------SSVSGHKGLTPTLTPSIVGTAEENAKVDI 373

Qy          67 YLDTRVILSLDV 78
               |:| ::: |:||
Db         374 YVDNKLVASVDV 385
```

RESULT 13
T38260
hypothetical protein SPAC23C4.05c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T38260
R;Harris, D.; Squares, R.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z21782
A;Accession: T38260
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-431 <HAR>
A;Cross-references: EMBL:Z99753; PIDN:CAB16876.1; GSPDB:GN00066; SPDB:SPAC23C4.05c
A;Experimental source: strain 972h-; cosmid c23C4
C;Genetics:
A;Gene: SPDB:SPAC23C4.05c
A;Map position: 1
A;Introns: 23/1

  Query Match 12.9%; Score 72; DB 2; Length 431;
  Best Local Similarity 23.6%; Pred. No. 18;
  Matches 21; Conservative 16; Mismatches 38; Indels 14; Gaps 2;

```
Qy          32 PQNSLETTPSSVTSESSSGTTTGPSASWSNSKASPYLDTRVILSLDV----------P 79
               |  : :    :| :    |   ||: ||   |   :|    : ||||           |
Db          43 PSTTTKYVQRTVYAGREKGKIGGPADSWPQRKLDDFLQNHGVKSLDVPPIETPSQFWRKP 102

Qy          80 IGLLRILLEQAR--YKAARNQAATNAQIL 106
               :  :   : :: :  |:  :| |: ||| |
Db         103 LQYVSKVTDKCKSFYEKEKNHASHNAQKL 131
```

RESULT 14
MNNZSP
nonstructural protein V - simian paramyxovirus SV5 (strain W3)
C;Species: simian paramyxovirus SV5
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 16-Jul-1999
C;Accession: A31594
R;Thomas, S.M.; Lamb, R.A.; Paterson, R.G.
Cell 54, 891-902, 1988
A;Title: Two mRNAs that differ by two nontemplated nucleotides encode the amino cotermina
A;Reference number: A90902; MUID:88311091; PMID:3044614
A;Accession: A31594
A;Molecule type: mRNA
A;Residues: 1-222 <THO>
A;Cross-references: GB:J03142; NID:g335118; PIDN:AAA47882.1; PID:g335119
C;Genetics:
A;Gene: V
C;Superfamily: simian paramyxovirus nonstructural protein V; V/P protein homology
C;Keywords: alternative splicing; metal binding; nonstructural protein
F;1-164/Domain: V/P protein homology <VPN>
F;190-211/Domain: metal binding #status predicted <MTB>

  Query Match 12.8%; Score 71.5; DB 1; Length 222;
  Best Local Similarity 32.3%; Pred. No. 8.9;
  Matches 31; Conservative 9; Mismatches 29; Indels 27; Gaps 5;

```
Qy          20 VPGTPIPTFQLLPQNSLETTPSSVTSESSSGTTTGPSASWSNSKASPY----LDTRVILS 75
               ||| |||     |   |::|||: |    || |  || |:   | : :    | || |
Db          93 VPGKPIPN----PLLGLDSTPSTQTVLDLSGKTL-PSGSYKGVKLAKFGKENLMTRFI-- 145

Qy          76 LDVPIGLLRILLEQARYKAARNQAATNAQILAHVGR 111
                  |: |    |  ||:: |    ||
Db         146 -----------EEPR----ENPIATSSPIDFKRGR 165
```

RESULT 15
T29689
hypothetical protein ZC266.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Sep-2000
C;Accession: T29689
R;Du, Z.; Kemp, K.; Scheet, P.
submitted to the EMBL Data Library, March 1996
A;Description: The sequence of C. elegans cosmid ZC266.
A;Reference number: Z20665
A;Accession: T29689
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA

A;Residues: 1-276 <DUZ>
A;Cross-references: EMBL:U53140; PIDN:AAA96101.1; GSPDB:GN00023; CESP:ZC266.2
A;Experimental source: strain Bristol N2; clone ZC266
C;Genetics:
A;Gene: CESP:ZC266.2
A;Map position: 5
A;Introns: 40/3; 66/1; 100/3; 133/1; 165/2
C;Superfamily: Caenorhabditis elegans hypothetical protein ZC266.2

Query Match 12.8%; Score 71.5; DB 2; Length 276;
Best Local Similarity 30.5%; Pred. No. 12;
Matches 29; Conservative 13; Mismatches 38; Indels 15; Gaps 4;

```
Qy          18 LFVPGTPIPTFQLLPQNSLETTPSSVTSESSSG-TTTGPSASWSNSKASPYLDTRVI--- 73
               ::  | | |   |   :|   | |   | :|:|  |   |:|:| ||   ||  ||:
Db         126 VYSEGCPSPDSSLKKFSSANVTISK--SRTSNGEVTISSSSSYSRSKRRQYL--RVLRRC 181

Qy          74 -------LSLDVPIGLLRILLEQARYKAARNQAAT 101
                    ||:::|  |||: |  :       | |
Db         182 LCITIFDLSMNLPSYLLRLYLSLSNEPVTEEWAET 216
```

Search completed: April 20, 2004, 18:57:22
Job time : 22.16 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 20, 2004, 18:50:27 ; Search time 74.6667 Seconds
(without alignments)
423.821 Million cell updates/sec

Title: US-09-919-473-10
Perfect score: 557
Sequence: 1 MTRWALVVFVVLMLDRILFV.....KAARNQAATNAQILAHVGRR 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	557	100.0	112	5	AAE21008	Aae21008 Mouse uro
2	312	56.0	112	5	AAE21006	Aae21006 Human uro
3	312	56.0	112	5	AAO15170	Aao15170 Human str
4	179	32.1	38	5	AAO19441	Aao19441 Murine ur
5	179	32.1	38	5	ABB82357	Abb82357 Mouse uro
6	145	26.0	41	5	AAE21007	Aae21007 Human mat
7	140	25.1	38	7	ADE64811	Ade64811 Corticotr
8	140	25.1	38	7	ADE51097	Ade51097 CRF2 non-
9	139	25.0	38	5	AAE21009	Aae21009 Human uro
10	139	25.0	38	5	AAO19442	Aao19442 Human uro
11	139	25.0	38	5	ABB82356	Abb82356 Human uro
12	139	25.0	38	7	ADE64820	Ade64820 Corticotr
13	139	25.0	38	7	ADE64701	Ade64701 CRF-2 rel
14	139	25.0	38	7	ADE65051	Ade65051 Corticotr
15	139	25.0	38	7	ADE51106	Ade51106 CRF2 non-
16	139	25.0	38	7	ADE51337	Ade51337 CRF2 non-
17	139	25.0	38	7	ADE50987	Ade50987 CRF2 huma
18	139	25.0	39	7	ADE65065	Ade65065 Corticotr
19	139	25.0	39	7	ADE65053	Ade65053 Corticotr
20	139	25.0	39	7	ADE51351	Ade51351 CRF2 non-
21	139	25.0	39	7	ADE51339	Ade51339 CRF2 non-
22	138	24.8	38	7	ADE64819	Ade64819 Corticotr
23	138	24.8	38	7	ADE51105	Ade51105 CRF2 non-
24	137	24.6	38	7	ADE64807	Ade64807 Corticotr
25	137	24.6	38	7	ADE51093	Ade51093 CRF2 non-
26	136	24.4	38	7	ADE64824	Ade64824 Corticotr
27	136	24.4	38	7	ADE64827	Ade64827 Corticotr
28	136	24.4	38	7	ADE64806	Ade64806 Corticotr
29	136	24.4	38	7	ADE64821	Ade64821 Corticotr
30	136	24.4	38	7	ADE51113	Ade51113 CRF2 non-
31	136	24.4	38	7	ADE51092	Ade51092 CRF2 non-
32	136	24.4	38	7	ADE51110	Ade51110 CRF2 non-
33	136	24.4	38	7	ADE51107	Ade51107 CRF2 non-
34	135	24.2	38	7	ADE64808	Ade64808 Corticotr
35	135	24.2	38	7	ADE64809	Ade64809 Corticotr
36	135	24.2	38	7	ADE64817	Ade64817 Corticotr
37	135	24.2	38	7	ADE64825	Ade64825 Corticotr
38	135	24.2	38	7	ADE51111	Ade51111 CRF2 non-
39	135	24.2	38	7	ADE51094	Ade51094 CRF2 non-
40	135	24.2	38	7	ADE51095	Ade51095 CRF2 non-
41	135	24.2	38	7	ADE51103	Ade51103 CRF2 non-
42	135	24.2	44	7	ADE64993	Ade64993 Corticotr
43	135	24.2	44	7	ADE51279	Ade51279 CRF2 non-
44	134	24.1	38	7	ADE64816	Ade64816 Corticotr
45	134	24.1	38	7	ADE64815	Ade64815 Corticotr

ALIGNMENTS

RESULT 1
AAE21008
ID AAE21008 standard; protein; 112 AA.
XX
AC AAE21008;
XX
DT 01-JUL-2002 (first entry)
XX
DE Mouse urocortin II (ucn) protein.
XX
KW Mouse; urocortin-related peptide; URP; antipyretic; cardiant; urocortin;
KW ucn; tranquilliser; appetite dysfunction; congestive heart failure;
KW stress; anxiety.
XX
OS Mus musculus.
XX
PN WO200212307-A1.
XX
PD 14-FEB-2002.
XX
PF 31-JUL-2001; 2001WO-US023976.
XX
PR 04-AUG-2000; 2000US-0223255P.
PR 07-MAR-2001; 2001US-0273969P.
XX
PA (RERE-) RES DEV FOUND.
XX
PI Vale WW, Sawchenko PF, Lewis KA, Vaughan JM, Reyes TM, Rivier JE;
PI Hogenesch JB, Perrin MH;
XX
DR WPI; 2002-241737/29.
XX
PT Novel urocortin II polypeptide or human urocortin-related peptide, for
PT treating high body temperature, appetite dysfunction, congestive heart
PT failure, stress, anxiety and low levels of adrenocortico tropic hormone.
XX
PS Claim 2; Fig 4A; 94pp; English.
XX
CC The invention relates to a modified protein selected from urocortin II
CC (Ucn II) and human urocortin-related peptide (URP). A pharmaceutical
CC composition is useful for treating a pathophysiological state including
CC high body temperature, appetite dysfunction, congestive heart failure,
CC stress, anxiety and undesirably low levels of adrenocortico tropic
CC hormone (ACTH) secretions. A modified protein conjugate is useful in
CC scintigraphy and in various assays, and also for the targetted
CC destruction of Corticotropin-releasing factor (CRF) receptor bearing
CC cells. The present sequence is mouse urocortin II (ucn) protein
XX

```
SQ   Sequence 112 AA;

  Query Match             100.0%;  Score 557;  DB 5;  Length 112;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-54;
  Matches  112;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MTRWALVVFVVLMLDRILFVPGTPIPTFQLLPQNSLETTPSSVTSESSSGTTTGPSASWS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MTRWALVVFVVLMLDRILFVPGTPIPTFQLLPQNSLETTPSSVTSESSSGTTTGPSASWS 60

Qy         61 NSKASPYLDTRVILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHVGRR 112
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NSKASPYLDTRVILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHVGRR 112


RESULT 2
AAE21006
ID   AAE21006 standard; protein; 112 AA.
XX
AC   AAE21006;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human urocortin-related peptide (URP) protein.
XX
KW   Human; urocortin-related peptide; URP; antipyretic; cardiant; urocortin;
KW   ucn; tranquilliser; appetite dysfunction; congestive heart failure;
KW   stress; anxiety.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .19
FT                   /label= Signal_peptide
FT   Protein         72. .112
FT                   /label= Mature_URP_protein
FT   Modified-site   112
FT                   /note= "C-terminal amide"
XX
PN   WO200212307-A1.
XX
PD   14-FEB-2002.
XX
PF   31-JUL-2001; 2001WO-US023976.
XX
PR   04-AUG-2000; 2000US-0223255P.
PR   07-MAR-2001; 2001US-0273969P.
XX
PA   (RERE-) RES DEV FOUND.
XX
PI   Vale WW,  Sawchenko PF,  Lewis KA,  Vaughan JM,  Reyes TM,  Rivier JE;
PI   Hogenesch JB,  Perrin MH;
XX
DR   WPI; 2002-241737/29.
DR   N-PSDB; AAD33401.
XX
PT   Novel urocortin II polypeptide or human urocortin-related peptide, for
PT   treating high body temperature, appetite dysfunction, congestive heart
PT   failure, stress, anxiety and low levels of adrenocortico tropic hormone.
XX
PS   Claim 18; Fig 1; 94pp; English.
XX
CC   The invention relates to a modified protein selected from urocortin II
CC   (Ucn II) and human urocortin-related peptide (URP). A pharmaceutical
CC   composition is useful for treating a pathophysiological state including
CC   high body temperature, appetite dysfunction, congestive heart failure,
CC   stress, anxiety and undesirably low levels of adrenocortico tropic
CC   hormone (ACTH) secretions. A modified protein conjugate is useful in
CC   scintigraphy and in various assays, and also for the targetted
CC   destruction of Corticotropin-releasing factor (CRF) receptor bearing
CC   cells. The present sequence is human URP protein
XX
SQ   Sequence 112 AA;

  Query Match             56.0%;  Score 312;  DB 5;  Length 112;
  Best Local Similarity   60.9%;  Pred. No. 5.7e-27;
  Matches   67;  Conservative   15;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          1 MTRWALVVFVVLMLDRILFVPGTPIPTFQLLPQNSLETTPSSVTSESSSGTTTGPSASWS 60
              |||  ||:: :|||| |:| || |||||||| |||| :|||    |||| |   | | |: |
Db          1 MTRCALLLLMVLMLGRVLVVPVTPIPTFQLRPQNSPQTTPRPAASESPSAAPTWPWAAQS 60

Qy         61 NSKASPYLDTRVILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHVG 110
              :   : :  :|::|||||||||:|||||| :||| || |||:||| ||
Db         61 HCSPTRHPGSRIVLSLDVPIGLLQILLEQARARAAREQATTNARILARVG 110


RESULT 3
AAO15170
ID   AAO15170 standard; protein; 112 AA.
XX
AC   AAO15170;
XX
DT   02-SEP-2002  (first entry)
XX
DE   Human stresscopin 1 protein.
XX
KW   Human; stresscopin 1; weight reduction; gene therapy;
KW   corticotropin releasing hormone receptor 2 activator; CRH-R2 activator;
KW   appetite suppression; cardioprotection; inflammation; heart disease;
KW   organ graft rejection; hypertension; trauma stress; dysthymia; oedema;
KW   skin disease; inflammatory arthritis; rheumatoid arthritis;
KW   non-infectious inflammatory arthropathy; stress-related disorder.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .66
FT                   /label= Signal_peptide
FT   Protein         67. .112
FT                   /note= "Mature stresscopin 1 protein"
FT   Misc-difference 67. .109
FT                   /note= "This region is illegible in the specification and
FT                   has been generated by decoding the corresponding
FT                   nucleotide (AAL43490)"
XX
PN   WO200234934-A2.
XX
PD   02-MAY-2002.
XX
PF   10-OCT-2001; 2001WO-US032065.
XX
PR   26-OCT-2000; 2000US-0244128P.
PR   15-MAR-2001; 2001US-0276615P.
XX
PA   (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
PI   Hsu SY,  Hsueh AJW;
XX
DR   WPI; 2002-471444/50.
DR   N-PSDB; AAL43490.
XX
PT   Composition comprising human stresscopin 1 or stresscopin 2 polypeptide,
PT   useful in appetite suppression, for cardioprotection, reducing edema,
PT   reducing inflammation, organ graft rejection, reducing hypertension.
XX
PS   Claim 2; Fig 1A; 50pp; English.
XX
CC   The invention comprises the amino acid and coding sequences of two human
CC   proteins which activate the corticotropin releasing hormone receptor 2
CC   (CRH-R2). The proteins of the invention are called stresscopin 1 and
CC   stresscopin 2. The stresscopin DNA and protein sequences of the invention
CC   are useful for appetite suppression, cardioprotection, reducing oedema,
CC   reducing inflammation, reducing organ graft rejection, reducing
CC   hypertension and reducing trauma stress. The stresscopin DNA and protein
CC   sequences are also useful for the treatment of dysthymia, skin diseases,
```

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CC   inflammatory arthritis, non-infectious inflammatory arthropathy (e.g.
CC   rheumatoid arthritis), heart disease and stress-related disorders. The
CC   present amino acid sequence represents the human stresscopin 1 protein
XX
SQ   Sequence 112 AA;

  Query Match             56.0%;  Score 312;  DB 5;  Length 112;
  Best Local Similarity   60.9%;  Pred. No. 5.7e-27;
  Matches   67;  Conservative   15;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          1 MTRWALVVFVVLMLDRILFVPGTPIPTFQLLPQNSLETTPSSVTSESSSGTTTGPSASWS 60
              ||| ||:: :|||| |:| || |||||||| |||| :|||    ||| |   | | |: |
Db          1 MTRCALLLLMVLMLGRVLVVPVTPIPTFQLRPQNSPQTTPRPAASESPSAAPTWPWAAQS 60

Qy         61 NSKASPYLDTRVILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHVG 110
              :   : :  :|::|||||||||||:|||||| :||| || |||:||| ||
Db         61 HCSPTRHPGSRIVLSLDVPIGLLQILLEQARARAAREQATTNARILARVG 110


RESULT 4
AAO19441
ID   AAO19441 standard; peptide; 38 AA.
XX
AC   AAO19441;
XX
DT   10-DEC-2002  (first entry)
XX
DE   Murine urocortin II.
XX
KW   Human; rat; mouse; sheep; cow; chicken; CRF1R; CRF2R;
KW   skeletal muscle atrophy; corticotrophin releasing factor-2 receptor;
KW   muscular dystrophy; corticotrophin releasing factor-1 receptor;
KW   gene therapy.
XX
OS   Mus musculus.
XX
PN   WO200269908-A2.
XX
PD   12-SEP-2002.
XX
PF   06-MAR-2002; 2002WO-US007476.
XX
PR   06-MAR-2001; 2001US-00799978.
XX
PA   (PROC ) PROCTER & GAMBLE CO.
XX
PI   Isfort RJ,  Sheldon RJ;
XX
DR   WPI; 2002-713413/77.
XX
PT   Identifying candidate compounds for regulating skeletal muscle mass or
PT   treating skeletal muscle atrophy by identifying test compounds that bind
PT   to, or activate, the corticotropin releasing factor-2 receptor.
XX
PS   Disclosure; Page 164; 167pp; English.
XX
CC   The present invention relates to a method of identifying candidate
CC   compounds for regulating skeletal muscle mass or function, and comprises
CC   contacting a test compound with a corticotropin releasing factor-2
CC   receptor (CRF2R) or with a cell expressing a functional CRF2R,
CC   determining whether the test compound binds to, or activates, the CRF2R
CC   and identifying the test compounds that bind to, or activates, the CRF2R
CC   as candidate compounds for regulating skeletal muscle mass or function.
CC   The method is useful for preparing a medicament for treating skeletal
CC   muscle atrophy or for prophylactic treatment of muscular dystrophies. The
CC   present sequence is a murine peptide shown in the invention
XX
SQ   Sequence 38 AA;

  Query Match             32.1%;  Score 179;  DB 5;  Length 38;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-12;
  Matches   38;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         72 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 109
              |||||||||||||||||||||||||||||||||||||
Db          1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38


RESULT 5
ABB82357
ID   ABB82357 standard; protein; 38 AA.
XX
AC   ABB82357;
XX
DT   08-JAN-2003  (first entry)
XX
DE   Mouse urocortin II protein (UcnII) fragment.
XX
KW   Urocortin III; Ucn-III; cardiant; antidiabetic; antimigraine; mouse;
KW   tranquilliser; antipyretic; vasotropic; gastrointestinal; antiangiogenic;
KW   vaccine; urocortin II; UcnII.
XX
OS   Mus musculus.
XX
PN   WO200274326-A2.
XX
PD   26-SEP-2002.
XX
PF   15-MAR-2002; 2002WO-US009115.
XX
PR   15-MAR-2001; 2001US-0276069P.
PR   31-MAY-2001; 2001US-0294914P.
XX
PA   (RERE-) RES DEV FOUND.
XX
PI   Vale WW,  Rivier JE,  Kunitake KS,  Lewis KA,  Perrin MH,  Gulyas J;
XX
DR   WPI; 2002-740838/80.
XX
PT   New human or mouse urocortin III protein, useful e.g. for treating
PT   congestive heart failure, vascular disease, gastrointestinal dysfunction,
PT   diabetes mellitus, high temperature, appetite dysfunction and stress.
XX
PS   Example; Fig 2C; 81pp; English.
XX
CC   The invention relates to an isolated and purified human or mouse
CC   urocortin III (Ucn-III) protein. The Ucn-III protein is is useful: (i)
CC   for treating a pathophysiological state including congestive heart
CC   failure, vascular disease, gastrointestinal dysfunction, diabetes
CC   mellitus, high temperature, appetite dysfunction, stress, undesirably low
CC   levels of glucagon secretion or activity, anxiety and migraine headaches;
CC   (ii) for determining whether a cell has urocortin III receptors; and
CC   (iii) for inhibiting angiogenesis. The present sequence represents the
CC   mouse urocortin II protein fragment
XX
SQ   Sequence 38 AA;

  Query Match             32.1%;  Score 179;  DB 5;  Length 38;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-12;
  Matches   38;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         72 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 109
              |||||||||||||||||||||||||||||||||||||
Db          1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38


RESULT 6
AAE21007
ID   AAE21007 standard; peptide; 41 AA.
XX
AC   AAE21007;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human mature urocortin-related peptide (URP).
XX
```

KW Human; urocortin-related peptide; URP; antipyretic; cardiant; urocortin;
KW ucn; tranquilliser; appetite dysfunction; congestive heart failure;
KW stress; anxiety.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 41
FT /note= "C-terminal amide"
XX
PN WO200212307-A1.
XX
PD 14-FEB-2002.
XX
PF 31-JUL-2001; 2001WO-US023976.
XX
PR 04-AUG-2000; 2000US-0223255P.
PR 07-MAR-2001; 2001US-0273969P.
XX
PA (RERE-) RES DEV FOUND.
XX
PI Vale WW, Sawchenko PF, Lewis KA, Vaughan JM, Reyes TM, Rivier JE;
PI Hogenesch JB, Perrin MH;
XX
DR WPI; 2002-241737/29.
DR N-PSDB; AAD33401.
XX
PT Novel urocortin II polypeptide or human urocortin-related peptide, for
PT treating high body temperature, appetite dysfunction, congestive heart
PT failure, stress, anxiety and low levels of adrenocortico tropic hormone.
XX
PS Claim 26; Page 30; 94pp; English.
XX
CC The invention relates to a modified protein selected from urocortin II
CC (Ucn II) and human urocortin-related peptide (URP). A pharmaceutical
CC composition is useful for treating a pathophysiological state including
CC high body temperature, appetite dysfunction, congestive heart failure,
CC stress, anxiety and undesirably low levels of adrenocortico tropic
CC hormone (ACTH) secretions. A modified protein conjugate is useful in
CC scintigraphy and in various assays, and also for the targetted
CC destruction of Corticotropin-releasing factor (CRF) receptor bearing
CC cells. The present sequence is mature human URP
XX
SQ Sequence 41 AA;

Query Match 26.0%; Score 145; DB 5; Length 41;
Best Local Similarity 76.9%; Pred. No. 8.4e-09;
Matches 30; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 72 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHVG 110
::|||||||||:|||||| :||| || |||:||| ||
Db 1 IVLSLDVPIGLLQILLEQARARAAREQATTNARILARVG 39

RESULT 7
ADE64811
ID ADE64811 standard; peptide; 38 AA.
XX
AC ADE64811;
XX
DT 29-JAN-2004 (first entry)
XX
DE Corticotropin-releasing factor-2 polypeptide, SEQ ID No 114.
XX
KW corticotropin-releasing factor-2; CRF2; myopathic; osteopathic;
KW hypotensive; cardiant; vasotropic; antimigraine; cerebroprotective;
KW nootropic; neuroprotective; anorectic; antidiabetic; analgesic;
KW antiallergic; tranquilizer; anxiolytic; antidepressant; antiarthritic;
KW gene therapy.
XX
OS Unidentified.
XX
PN WO2003062277-A1.
XX
PD 31-JUL-2003.
XX
PF 16-JAN-2003; 2003WO-US001454.
XX
PR 16-JAN-2002; 2002US-0349117P.
PR 29-APR-2002; 2002US-0376337P.
PR 14-JUN-2002; 2002US-0388895P.
PR 19-SEP-2002; 2002US-0411988P.
XX
PA (PROC) PROCTER & GAMBLE CO.
XX
PI Isfort RJ, Mazur WA;
XX
DR WPI; 2003-787975/74.
XX
PT New non-native peptide derived from corticotropin-releasing factor-2,
PT useful for treatment and prevention of e.g. muscular atrophy, also
PT related nucleic acid and antibodies.
XX
PS Example 2; SEQ ID NO 114; 304pp; English.
XX
CC The invention relates to a novel non-native peptide derived from
CC corticotropin-releasing factor-2 (CRF2). The CRF2 peptides have the
CC following activities: myopathic, osteopathic, hypotensive, cardiant,
CC vasotropic, antimigraine, cerebroprotective, nootropic, neuroprotective,
CC anorectic, antidiabetic, analgesic, antiallergic, tranquilizer,
CC anxiolytic, antidepressant, and antiarthritic. The CRF2 peptides, and
CC related compounds derived from other proteins, are used to prevent or
CC treat disorders modulated by the CRF2 receptor, e.g. skeletal muscle
CC atrophy or wasting, and bone disorders, however caused; heart/circulatory
CC diseases (e.g. hypertension, congestive heart failure, heart attack,
CC reperfusion injury, migraine, stroke, memory loss, Alzheimer's disease,
CC dementia); joint disorders (osteoarthritis or rheumatoid arthritis);
CC metabolic disease (obesity or diabetes); pain; allergy; stress; anxiety;
CC low levels of adrenocorticotrophic hormone; anorexia nervosa; depression;
CC also to reduce body temperature and to control appetite or cognitive
CC function. Nucleic acids, optionally labelled, that encode the CRF2
CC peptides are used as primers and probes for amplification, also for gene
CC synthesis and for recombinant production of CRF2 peptides, including use
CC in gene therapy. Antibodies specific for the CRF2 peptides are used to
CC evaluate expression of the CRF2 peptides after gene therapy. This
CC sequence represents a novel native CRF polypeptide of the invention.
XX
SQ Sequence 38 AA;

Query Match 25.1%; Score 140; DB 7; Length 38;
Best Local Similarity 76.3%; Pred. No. 2.8e-08;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 72 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 109
::|||||||||:|||||| :||| || |||:||| |
Db 1 IVLSLDVPIGLLQILLEQARQRAAREQATTNARILARV 38

RESULT 8
ADE51097
ID ADE51097 standard; peptide; 38 AA.
XX
AC ADE51097;
XX
DT 29-JAN-2004 (first entry)
XX
DE CRF2 non-native polypeptide, SEQ ID No 114.
XX
KW non-native; corticotropin-releasing factor-2; CRF2; myopathic;
KW osteopathic; hypotensive; cardiant; vasotropic; antimigraine;
KW cerebroprotective; nootropic; neuroprotective; anorectic; antidiabetic;
KW analgesic; antiallergic; tranquilizer; anxiolytic; antidepressant;
KW antiarthritic.
XX
OS Unidentified.
XX

PN WO2003062268-A2.
XX
PD 31-JUL-2003.
XX
PF 16-JAN-2003; 2003WO-US001451.
XX
PR 16-JAN-2002; 2002US-0349117P.
PR 29-APR-2002; 2002US-0376337P.
PR 14-JUN-2002; 2002US-0388895P.
PR 19-SEP-2002; 2002US-0411988P.
XX
PA (PROC) PROCTER & GAMBLE CO.
XX
PI Isfort RJ, Mazur WA;
XX
DR WPI; 2003-787974/74.
XX
PT New non-native peptide derived from corticotropin-releasing factor-2,
PT useful for treatment and prevention of e.g. muscular atrophy, also
PT related nucleic acid and antibodies.
XX
PS Example 2; SEQ ID NO 114; 300pp; English.
XX
CC The invention relates to a novel non-native peptide derived from
CC corticotropin-releasing factor-2 (CRF2). The non-native CRF2 peptides
CC have the following activities: myopathic, osteopathic, hypotensive,
CC cardiant, vasotropic, antimigraine, cerebroprotective, nootropic,
CC neuroprotective, anorectic, antidiabetic, analgesic, antiallergic,
CC tranquilizer, anxiolytic, antidepressant, and antiarthritic. The non-
CC native CRF2 peptides, and related compounds derived from other proteins,
CC are used to prevent or treat disorders modulated by the CRF2 receptor,
CC e.g. skeletal muscle atrophy or wasting, and bone disorders, however
CC caused; heart/circulatory diseases (e.g. hypertension, congestive heart
CC failure, heart attack, reperfusion injury, migraine, stroke, memory loss,
CC Alzheimer's diseases, dementia); joint disorders (osteoarthritis or
CC rheumatoid arthritis); metabolic disease (obesity or diabetes); pain;
CC allergy; stress; anxiety; low levels of adrenocorticotrophic hormone;
CC anorexia nervosa; depression; also to reduce body temperature and to
CC control appetite or cognitive function. Nucleic acids, optionally
CC labelled, that encode the non-native CRF2 peptides are used as primers
CC and probes for amplification, also for gene synthesis and for recombinant
CC production of the non-native CRF2 peptides, including use in gene
CC therapy. Antibodies specific for the non-native CRF2 peptides are used to
CC evaluate expression of the non-native CRF2 peptides after gene therapy.
CC This sequence represents a CRF2 non-native polypeptide of the invention.
XX
SQ Sequence 38 AA;

Query Match 25.1%; Score 140; DB 7; Length 38;
Best Local Similarity 76.3%; Pred. No. 2.8e-08;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

```
Qy         72 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 109
              ::|||||||||||:|||||||  :|||  ||  |||:|||  |
Db          1 IVLSLDVPIGLLQILLEQARQRAAREQATTNARILARV 38
```

RESULT 9
AAE21009
ID AAE21009 standard; peptide; 38 AA.
XX
AC AAE21009;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human urocortin-related peptide (URP).
XX
KW Human; urocortin-related peptide; URP; antipyretic; cardiant; urocortin;
KW ucn; tranquilliser; appetite dysfunction; congestive heart failure;
KW stress; anxiety.
XX
OS Homo sapiens.
XX

FH Key Location/Qualifiers
FT Modified-site 38
FT /note= "C-terminal amide"
XX
PN WO200212307-A1.
XX
PD 14-FEB-2002.
XX
PF 31-JUL-2001; 2001WO-US023976.
XX
PR 04-AUG-2000; 2000US-0223255P.
PR 07-MAR-2001; 2001US-0273969P.
XX
PA (RERE-) RES DEV FOUND.
XX
PI Vale WW, Sawchenko PF, Lewis KA, Vaughan JM, Reyes TM, Rivier JE;
PI Hogenesch JB, Perrin MH;
XX
DR WPI; 2002-241737/29.
XX
PT Novel urocortin II polypeptide or human urocortin-related peptide, for
PT treating high body temperature, appetite dysfunction, congestive heart
PT failure, stress, anxiety and low levels of adrenocortico tropic hormone.
XX
PS Claim 36; Fig 4b; 94pp; English.
XX
CC The invention relates to a modified protein selected from urocortin II
CC (Ucn II) and human urocortin-related peptide (URP). A pharmaceutical
CC composition is useful for treating a pathophysiological state including
CC high body temperature, appetite dysfunction, congestive heart failure,
CC stress, anxiety and undesirably low levels of adrenocortico tropic
CC hormone (ACTH) secretions. A modified protein conjugate is useful in
CC scintigraphy and in various assays, and also for the targetted
CC destruction of Corticotropin-releasing factor (CRF) receptor bearing
CC cells. The present sequence is human URP
XX
SQ Sequence 38 AA;

Query Match 25.0%; Score 139; DB 5; Length 38;
Best Local Similarity 76.3%; Pred. No. 3.6e-08;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

```
Qy         72 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 109
              ::|||||||||||:|||||||  :|||  ||  |||:|||  |
Db          1 IVLSLDVPIGLLQILLEQARARAAREQATTNARILARV 38
```

RESULT 10
AAO19442
ID AAO19442 standard; peptide; 38 AA.
XX
AC AAO19442;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human urocortin-related peptide.
XX
KW Human; rat; mouse; sheep; cow; chicken; CRF1R; CRF2R;
KW skeletal muscle atrophy; corticotrophin releasing factor-2 receptor;
KW muscular dystrophy; corticotrophin releasing factor-1 receptor;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN WO200269908-A2.
XX
PD 12-SEP-2002.
XX
PF 06-MAR-2002; 2002WO-US007476.
XX
PR 06-MAR-2001; 2001US-00799978.
XX
PA (PROC) PROCTER & GAMBLE CO.

XX
PI Isfort RJ, Sheldon RJ;
XX
DR WPI; 2002-713413/77.
XX
PT Identifying candidate compounds for regulating skeletal muscle mass or
PT treating skeletal muscle atrophy by identifying test compounds that bind
PT to, or activate, the corticotropin releasing factor-2 receptor.
XX
PS Disclosure; Page 164; 167pp; English.
XX
CC The present invention relates to a method of identifying candidate
CC compounds for regulating skeletal muscle mass or function, and comprises
CC contacting a test compound with a corticotropin releasing factor-2
CC receptor (CRF2R) or with a cell expressing a functional CRF2R,
CC determining whether the test compound binds to, or activates, the CRF2R
CC and identifying the test compounds that bind to, or activates, the CRF2R
CC as candidate compounds for regulating skeletal muscle mass or function.
CC The method is useful for preparing a medicament for treating skeletal
CC muscle atrophy or for prophylactic treatment of muscular dystrophies. The
CC present sequence is a human peptide shown in the invention
XX
SQ Sequence 38 AA;

Query Match 25.0%; Score 139; DB 5; Length 38;
Best Local Similarity 76.3%; Pred. No. 3.6e-08;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 72 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 109
::|||||||||||:|||||||:|||||||:|||:|||
Db 1 IVLSLDVPIGLLQILLEQARARAAREQATTNARILARV 38

RESULT 11
ABB82356
ID ABB82356 standard; protein; 38 AA.
XX
AC ABB82356;
XX
DT 08-JAN-2003 (first entry)
XX
DE Human urocortin II protein (URP) fragment.
XX
KW Urocortin III; Ucn-III; cardiant; antidiabetic; antimigraine; human;
KW tranquilliser; antipyretic; vasotropic; gastrointestinal; antiangiogenic;
KW vaccine; urocortin II; URP.
XX
OS Homo sapiens.
XX
PN WO200274326-A2.
XX
PD 26-SEP-2002.
XX
PF 15-MAR-2002; 2002WO-US009115.
XX
PR 15-MAR-2001; 2001US-0276069P.
PR 31-MAY-2001; 2001US-0294914P.
XX
PA (RERE-) RES DEV FOUND.
XX
PI Vale WW, Rivier JE, Kunitake KS, Lewis KA, Perrin MH, Gulyas J;
XX
DR WPI; 2002-740838/80.
XX
PT New human or mouse urocortin III protein, useful e.g. for treating
PT congestive heart failure, vascular disease, gastrointestinal dysfunction,
PT diabetes mellitus, high temperature, appetite dysfunction and stress.
XX
PS Example; Fig 2C; 81pp; English.
XX
CC The invention relates to an isolated and purified human or mouse
CC urocortin III (Ucn-III) protein. The Ucn-III protein is is useful: (i)
CC for treating a pathophysiological state including congestive heart
CC failure, vascular disease, gastrointestinal dysfunction, diabetes
CC mellitus, high temperature, appetite dysfunction, stress, undesirably low
CC levels of glucagon secretion or activity, anxiety and migraine headaches;
CC (ii) for determining whether a cell has urocortin III receptors; and
CC (iii) for inhibiting angiogenesis. The present sequence represents the
CC human urocortin II protein fragment
XX
SQ Sequence 38 AA;

Query Match 25.0%; Score 139; DB 5; Length 38;
Best Local Similarity 76.3%; Pred. No. 3.6e-08;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 72 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 109
::|||||||||||:|||||||:|||||||:|||:|||
Db 1 IVLSLDVPIGLLQILLEQARARAAREQATTNARILARV 38

RESULT 12
ADE64820
ID ADE64820 standard; peptide; 38 AA.
XX
AC ADE64820;
XX
DT 29-JAN-2004 (first entry)
XX
DE Corticotropin-releasing factor-2 polypeptide, SEQ ID No 123.
XX
KW corticotropin-releasing factor-2; CRF2; myopathic; osteopathic;
KW hypotensive; cardiant; vasotropic; antimigraine; cerebroprotective;
KW nootropic; neuroprotective; anorectic; antidiabetic; analgesic;
KW antiallergic; tranquilizer; anxiolytic; antidepressant; antiarthritic;
KW gene therapy.
XX
OS Unidentified.
XX
PN WO2003062277-A1.
XX
PD 31-JUL-2003.
XX
PF 16-JAN-2003; 2003WO-US001454.
XX
PR 16-JAN-2002; 2002US-0349117P.
PR 29-APR-2002; 2002US-0376337P.
PR 14-JUN-2002; 2002US-0388895P.
PR 19-SEP-2002; 2002US-0411988P.
XX
PA (PROC) PROCTER & GAMBLE CO.
XX
PI Isfort RJ, Mazur WA;
XX
DR WPI; 2003-787975/74.
XX
PT New non-native peptide derived from corticotropin-releasing factor-2,
PT useful for treatment and prevention of e.g. muscular atrophy, also
PT related nucleic acid and antibodies.
XX
PS Example 2; SEQ ID NO 123; 304pp; English.
XX
CC The invention relates to a novel non-native peptide derived from
CC corticotropin-releasing factor-2 (CRF2). The CRF2 peptides have the
CC following activities: myopathic, osteopathic, hypotensive, cardiant,
CC vasotropic, antimigraine, cerebroprotective, nootropic, neuroprotective,
CC anorectic, antidiabetic, analgesic, antiallergic, tranquilizer,
CC anxiolytic, antidepressant, and antiarthritic. The CRF2 peptides, and
CC related compounds derived from other proteins, are used to prevent or
CC treat disorders modulated by the CRF2 receptor, e.g. skeletal muscle
CC atrophy or wasting, and bone disorders, however caused; heart/circulatory
CC diseases (e.g. hypertension, congestive heart failure, heart attack,
CC reperfusion injury, migraine, stroke, memory loss, Alzheimer's disease,
CC dementia); joint disorders (osteoarthritis or rheumatoid arthritis);
CC metabolic disease (obesity or diabetes); pain; allergy; stress; anxiety;
CC low levels of adrenocorticotrophic hormone; anorexia nervosa; depression;

CC also to reduce body temperature and to control appetite or cognitive
CC function. Nucleic acids, optionally labelled, that encode the CRF2
CC peptides are used as primers and probes for amplification, also for gene
CC synthesis and for recombinant production of CRF2 peptides, including use
CC in gene therapy. Antibodies specific for the CRF2 peptides are used to
CC evaluate expression of the CRF2 peptides after gene therapy. This
CC sequence represents a novel native CRF polypeptide of the invention.
XX
SQ Sequence 38 AA;

Query Match 25.0%; Score 139; DB 7; Length 38;
Best Local Similarity 76.3%; Pred. No. 3.6e-08;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 72 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 109
::|||||||||||:|||||||:|||||||:|||:||| |
Db 1 IVLSLDVPIGLLQILLEQARQEAAREQATTNARILARV 38

RESULT 13
ADE64701
ID ADE64701 standard; peptide; 38 AA.
XX
AC ADE64701;
XX
DT 29-JAN-2004 (first entry)
XX
DE CRF-2 related human urocortin II polypeptide, SEQ ID No 4.
XX
KW corticotropin-releasing factor-2; CRF2; myopathic; osteopathic;
KW hypotensive; cardiant; vasotropic; antimigraine; cerebroprotective;
KW nootropic; neuroprotective; anorectic; antidiabetic; analgesic;
KW antiallergic; tranquilizer; anxiolytic; antidepressant; antiarthritic;
KW gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO2003062277-A1.
XX
PD 31-JUL-2003.
XX
PF 16-JAN-2003; 2003WO-US001454.
XX
PR 16-JAN-2002; 2002US-0349117P.
PR 29-APR-2002; 2002US-0376337P.
PR 14-JUN-2002; 2002US-0388895P.
PR 19-SEP-2002; 2002US-0411988P.
XX
PA (PROC) PROCTER & GAMBLE CO.
XX
PI Isfort RJ, Mazur WA;
XX
DR WPI; 2003-787975/74.
XX
PT New non-native peptide derived from corticotropin-releasing factor-2,
PT useful for treatment and prevention of e.g. muscular atrophy, also
PT related nucleic acid and antibodies.
XX
PS Example 1; SEQ ID NO 4; 304pp; English.
XX
CC The invention relates to a novel non-native peptide derived from
CC corticotropin-releasing factor-2 (CRF2). The CRF2 peptides have the
CC following activities: myopathic, osteopathic, hypotensive, cardiant,
CC vasotropic, antimigraine, cerebroprotective, nootropic, neuroprotective,
CC anorectic, antidiabetic, analgesic, antiallergic, tranquilizer,
CC anxiolytic, antidepressant, and antiarthritic. The CRF2 peptides, and
CC related compounds derived from other proteins, are used to prevent or
CC treat disorders modulated by the CRF2 receptor, e.g. skeletal muscle
CC atrophy or wasting, and bone disorders, however caused; heart/circulatory
CC diseases (e.g. hypertension, congestive heart failure, heart attack,
CC reperfusion injury, migraine, stroke, memory loss, Alzheimer's disease,
CC dementia); joint disorders (osteoarthritis or rheumatoid arthritis);
CC metabolic disease (obesity or diabetes); pain; allergy; stress; anxiety;
CC low levels of adrenocorticotrophic hormone; anorexia nervosa; depression;
CC also to reduce body temperature and to control appetite or cognitive
CC function. Nucleic acids, optionally labelled, that encode the CRF2
CC peptides are used as primers and probes for amplification, also for gene
CC synthesis and for recombinant production of CRF2 peptides, including use
CC in gene therapy. Antibodies specific for the CRF2 peptides are used to
CC evaluate expression of the CRF2 peptides after gene therapy. This
CC sequence represents a novel native CRF polypeptide of the invention.
XX
SQ Sequence 38 AA;

Query Match 25.0%; Score 139; DB 7; Length 38;
Best Local Similarity 76.3%; Pred. No. 3.6e-08;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 72 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 109
::|||||||||||:|||||||:|||||||:|||:||| |
Db 1 IVLSLDVPIGLLQILLEQARARAAREQATTNARILARV 38

RESULT 14
ADE65051
ID ADE65051 standard; peptide; 38 AA.
XX
AC ADE65051;
XX
DT 29-JAN-2004 (first entry)
XX
DE Corticotropin-releasing factor-2 polypeptide, SEQ ID No 354.
XX
KW corticotropin-releasing factor-2; CRF2; myopathic; osteopathic;
KW hypotensive; cardiant; vasotropic; antimigraine; cerebroprotective;
KW nootropic; neuroprotective; anorectic; antidiabetic; analgesic;
KW antiallergic; tranquilizer; anxiolytic; antidepressant; antiarthritic;
KW gene therapy.
XX
OS Unidentified.
XX
PN WO2003062277-A1.
XX
PD 31-JUL-2003.
XX
PF 16-JAN-2003; 2003WO-US001454.
XX
PR 16-JAN-2002; 2002US-0349117P.
PR 29-APR-2002; 2002US-0376337P.
PR 14-JUN-2002; 2002US-0388895P.
PR 19-SEP-2002; 2002US-0411988P.
XX
PA (PROC) PROCTER & GAMBLE CO.
XX
PI Isfort RJ, Mazur WA;
XX
DR WPI; 2003-787975/74.
XX
PT New non-native peptide derived from corticotropin-releasing factor-2,
PT useful for treatment and prevention of e.g. muscular atrophy, also
PT related nucleic acid and antibodies.
XX
PS Example 2; SEQ ID NO 354; 304pp; English.
XX
CC The invention relates to a novel non-native peptide derived from
CC corticotropin-releasing factor-2 (CRF2). The CRF2 peptides have the
CC following activities: myopathic, osteopathic, hypotensive, cardiant,
CC vasotropic, antimigraine, cerebroprotective, nootropic, neuroprotective,
CC anorectic, antidiabetic, analgesic, antiallergic, tranquilizer,
CC anxiolytic, antidepressant, and antiarthritic. The CRF2 peptides, and
CC related compounds derived from other proteins, are used to prevent or
CC treat disorders modulated by the CRF2 receptor, e.g. skeletal muscle
CC atrophy or wasting, and bone disorders, however caused; heart/circulatory
CC diseases (e.g. hypertension, congestive heart failure, heart attack,
CC reperfusion injury, migraine, stroke, memory loss, Alzheimer's disease,
CC dementia); joint disorders (osteoarthritis or rheumatoid arthritis);

CC metabolic disease (obesity or diabetes); pain; allergy; stress; anxiety;
CC low levels of adrenocorticotrophic hormone; anorexia nervosa; depression;
CC also to reduce body temperature and to control appetite or cognitive
CC function. Nucleic acids, optionally labelled, that encode the CRF2
CC peptides are used as primers and probes for amplification, also for gene
CC synthesis and for recombinant production of CRF2 peptides, including use
CC in gene therapy. Antibodies specific for the CRF2 peptides are used to
CC evaluate expression of the CRF2 peptides after gene therapy. This
CC sequence represents a novel native CRF polypeptide of the invention.
XX
SQ Sequence 38 AA;

Query Match 25.0%; Score 139; DB 7; Length 38;
Best Local Similarity 76.3%; Pred. No. 3.6e-08;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 72 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 109
::|||||||||||:|||||||:|||||||:|||:|||||
Db 1 IVLSLDVPIGLLQILLEQARARAAREQATTNARILARV 38

RESULT 15
ADE51106
ID ADE51106 standard; peptide; 38 AA.
XX
AC ADE51106;
XX
DT 29-JAN-2004 (first entry)
XX
DE CRF2 non-native polypeptide, SEQ ID No 123.
XX
KW non-native; corticotropin-releasing factor-2; CRF2; myopathic;
KW osteopathic; hypotensive; cardiant; vasotropic; antimigraine;
KW cerebroprotective; nootropic; neuroprotective; anorectic; antidiabetic;
KW analgesic; antiallergic; tranquilizer; anxiolytic; antidepressant;
KW antiarthritic.
XX
OS Unidentified.
XX
PN WO2003062268-A2.
XX
PD 31-JUL-2003.
XX
PF 16-JAN-2003; 2003WO-US001451.
XX
PR 16-JAN-2002; 2002US-0349117P.
PR 29-APR-2002; 2002US-0376337P.
PR 14-JUN-2002; 2002US-0388895P.
PR 19-SEP-2002; 2002US-0411988P.
XX
PA (PROC) PROCTER & GAMBLE CO.
XX
PI Isfort RJ, Mazur WA;
XX
DR WPI; 2003-787974/74.
XX
PT New non-native peptide derived from corticotropin-releasing factor-2,
PT useful for treatment and prevention of e.g. muscular atrophy, also
PT related nucleic acid and antibodies.
XX
PS Example 2; SEQ ID NO 123; 300pp; English.
XX
CC The invention relates to a novel non-native peptide derived from
CC corticotropin-releasing factor-2 (CRF2). The non-native CRF2 peptides
CC have the following activities: myopathic, osteopathic, hypotensive,
CC cardiant, vasotropic, antimigraine, cerebroprotective, nootropic,
CC neuroprotective, anorectic, antidiabetic, analgesic, antiallergic,
CC tranquilizer, anxiolytic, antidepressant, and antiarthritic. The non-
CC native CRF2 peptides, and related compounds derived from other proteins,
CC are used to prevent or treat disorders modulated by the CRF2 receptor,
CC e.g. skeletal muscle atrophy or wasting, and bone disorders, however
CC caused; heart/circulatory diseases (e.g. hypertension, congestive heart
CC failure, heart attack, reperfusion injury, migraine, stroke, memory loss,
CC Alzheimer's diseases, dementia); joint disorders (osteoarthritis or
CC rheumatoid arthritis); metabolic disease (obesity or diabetes); pain;
CC allergy; stress; anxiety; low levels of adrenocorticotrophic hormone;
CC anorexia nervosa; depression; also to reduce body temperature and to
CC control appetite or cognitive function. Nucleic acids, optionally
CC labelled, that encode the non-native CRF2 peptides are used as primers
CC and probes for amplification, also for gene synthesis and for recombinant
CC production of the non-native CRF2 peptides, including use in gene
CC therapy. Antibodies specific for the non-native CRF2 peptides are used to
CC evaluate expression of the non-native CRF2 peptides after gene therapy.
CC This sequence represents a CRF2 non-native polypeptide of the invention.
XX
SQ Sequence 38 AA;

Query Match 25.0%; Score 139; DB 7; Length 38;
Best Local Similarity 76.3%; Pred. No. 3.6e-08;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 72 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 109
::|||||||||||:|||||||:|||||||:|||:|||||
Db 1 IVLSLDVPIGLLQILLEQARQEAAREQATTNARILARV 38

Search completed: April 20, 2004, 18:54:43
Job time : 75.6667 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 20, 2004, 18:50:27 ; Search time 25.3333 Seconds
(without alignments)
423.821 Million cell updates/sec

Title: US-09-919-473-11
Perfect score: 179
Sequence: 1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	179	100.0	38	5	AAO19441	Aao19441 Murine ur
2	179	100.0	38	5	ABB82357	Abb82357 Mouse uro
3	179	100.0	112	5	AAE21008	Aae21008 Mouse uro
4	140	78.2	38	7	ADE64811	Ade64811 Corticotr
5	140	78.2	38	7	ADE51097	Ade51097 CRF2 non-
6	139	77.7	38	5	AAE21009	Aae21009 Human uro
7	139	77.7	38	5	AAO19442	Aao19442 Human uro
8	139	77.7	38	5	ABB82356	Abb82356 Human uro
9	139	77.7	38	7	ADE64820	Ade64820 Corticotr
10	139	77.7	38	7	ADE64701	Ade64701 CRF-2 rel
11	139	77.7	38	7	ADE65051	Ade65051 Corticotr
12	139	77.7	38	7	ADE51106	Ade51106 CRF2 non-
13	139	77.7	38	7	ADE51337	Ade51337 CRF2 non-
14	139	77.7	38	7	ADE50987	Ade50987 CRF2 huma
15	139	77.7	39	7	ADE65065	Ade65065 Corticotr
16	139	77.7	39	7	ADE65053	Ade65053 Corticotr
17	139	77.7	39	7	ADE51351	Ade51351 CRF2 non-
18	139	77.7	39	7	ADE51339	Ade51339 CRF2 non-
19	139	77.7	41	5	AAE21007	Aae21007 Human mat
20	139	77.7	112	5	AAE21006	Aae21006 Human uro
21	139	77.7	112	5	AAO15170	Aao15170 Human str
22	138	77.1	38	7	ADE64819	Ade64819 Corticotr
23	138	77.1	38	7	ADE51105	Ade51105 CRF2 non-
24	137	76.5	38	7	ADE64807	Ade64807 Corticotr
25	137	76.5	38	7	ADE51093	Ade51093 CRF2 non-
26	136	76.0	38	7	ADE64824	Ade64824 Corticotr
27	136	76.0	38	7	ADE64827	Ade64827 Corticotr
28	136	76.0	38	7	ADE64806	Ade64806 Corticotr
29	136	76.0	38	7	ADE64821	Ade64821 Corticotr
30	136	76.0	38	7	ADE51113	Ade51113 CRF2 non-
31	136	76.0	38	7	ADE51092	Ade51092 CRF2 non-
32	136	76.0	38	7	ADE51110	Ade51110 CRF2 non-
33	136	76.0	38	7	ADE51107	Ade51107 CRF2 non-
34	135	75.4	38	7	ADE64808	Ade64808 Corticotr
35	135	75.4	38	7	ADE64809	Ade64809 Corticotr
36	135	75.4	38	7	ADE64817	Ade64817 Corticotr
37	135	75.4	38	7	ADE64825	Ade64825 Corticotr
38	135	75.4	38	7	ADE51111	Ade51111 CRF2 non-
39	135	75.4	38	7	ADE51094	Ade51094 CRF2 non-
40	135	75.4	38	7	ADE51095	Ade51095 CRF2 non-
41	135	75.4	38	7	ADE51103	Ade51103 CRF2 non-
42	135	75.4	44	7	ADE64993	Ade64993 Corticotr
43	135	75.4	44	7	ADE51279	Ade51279 CRF2 non-
44	134	74.9	38	7	ADE64816	Ade64816 Corticotr
45	134	74.9	38	7	ADE64815	Ade64815 Corticotr

ALIGNMENTS

RESULT 1
AAO19441
ID AAO19441 standard; peptide; 38 AA.
XX
AC AAO19441;
XX
DT 10-DEC-2002 (first entry)
XX
DE Murine urocortin II.
XX
KW Human; rat; mouse; sheep; cow; chicken; CRF1R; CRF2R;
KW skeletal muscle atrophy; corticotrophin releasing factor-2 receptor;
KW muscular dystrophy; corticotrophin releasing factor-1 receptor;
KW gene therapy.
XX
OS Mus musculus.
XX
PN WO200269908-A2.
XX
PD 12-SEP-2002.
XX
PF 06-MAR-2002; 2002WO-US007476.
XX
PR 06-MAR-2001; 2001US-00799978.
XX
PA (PROC) PROCTER & GAMBLE CO.
XX
PI Isfort RJ, Sheldon RJ;
XX
DR WPI; 2002-713413/77.
XX
PT Identifying candidate compounds for regulating skeletal muscle mass or
PT treating skeletal muscle atrophy by identifying test compounds that bind
PT to, or activate, the corticotropin releasing factor-2 receptor.
XX
PS Disclosure; Page 164; 167pp; English.
XX
CC The present invention relates to a method of identifying candidate
CC compounds for regulating skeletal muscle mass or function, and comprises
CC contacting a test compound with a corticotropin releasing factor-2
CC receptor (CRF2R) or with a cell expressing a functional CRF2R,
CC determining whether the test compound binds to, or activates, the CRF2R
CC and identifying the test compounds that bind to, or activates, the CRF2R
CC as candidate compounds for regulating skeletal muscle mass or function.
CC The method is useful for preparing a medicament for treating skeletal
CC muscle atrophy or for prophylactic treatment of muscular dystrophies. The
CC present sequence is a murine peptide shown in the invention
XX

SQ Sequence 38 AA;

Query Match 100.0%; Score 179; DB 5; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.4e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
Db 1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38

RESULT 2
ABB82357
ID ABB82357 standard; protein; 38 AA.
XX
AC ABB82357;
XX
DT 08-JAN-2003 (first entry)
XX
DE Mouse urocortin II protein (UcnII) fragment.
XX
KW Urocortin III; Ucn-III; cardiant; antidiabetic; antimigraine; mouse;
KW tranquilliser; antipyretic; vasotropic; gastrointestinal; antiangiogenic;
KW vaccine; urocortin II; UcnII.
XX
OS Mus musculus.
XX
PN WO200274326-A2.
XX
PD 26-SEP-2002.
XX
PF 15-MAR-2002; 2002WO-US009115.
XX
PR 15-MAR-2001; 2001US-0276069P.
PR 31-MAY-2001; 2001US-0294914P.
XX
PA (RERE-) RES DEV FOUND.
XX
PI Vale WW, Rivier JE, Kunitake KS, Lewis KA, Perrin MH, Gulyas J;
XX
DR WPI; 2002-740838/80.
XX
PT New human or mouse urocortin III protein, useful e.g. for treating
PT congestive heart failure, vascular disease, gastrointestinal dysfunction,
PT diabetes mellitus, high temperature, appetite dysfunction and stress.
XX
PS Example; Fig 2C; 81pp; English.
XX
CC The invention relates to an isolated and purified human or mouse
CC urocortin III (Ucn-III) protein. The Ucn-III protein is is useful: (i)
CC for treating a pathophysiological state including congestive heart
CC failure, vascular disease, gastrointestinal dysfunction, diabetes
CC mellitus, high temperature, appetite dysfunction, stress, undesirably low
CC levels of glucagon secretion or activity, anxiety and migraine headaches;
CC (ii) for determining whether a cell has urocortin III receptors; and
CC (iii) for inhibiting angiogenesis. The present sequence represents the
CC mouse urocortin II protein fragment
XX
SQ Sequence 38 AA;

Query Match 100.0%; Score 179; DB 5; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.4e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
Db 1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38

RESULT 3
AAE21008
ID AAE21008 standard; protein; 112 AA.
XX
AC AAE21008;
XX
DT 01-JUL-2002 (first entry)
XX
DE Mouse urocortin II (ucn) protein.
XX
KW Mouse; urocortin-related peptide; URP; antipyretic; cardiant; urocortin;
KW ucn; tranquilliser; appetite dysfunction; congestive heart failure;
KW stress; anxiety.
XX
OS Mus musculus.
XX
PN WO200212307-A1.
XX
PD 14-FEB-2002.
XX
PF 31-JUL-2001; 2001WO-US023976.
XX
PR 04-AUG-2000; 2000US-0223255P.
PR 07-MAR-2001; 2001US-0273969P.
XX
PA (RERE-) RES DEV FOUND.
XX
PI Vale WW, Sawchenko PF, Lewis KA, Vaughan JM, Reyes TM, Rivier JE;
PI Hogenesch JB, Perrin MH;
XX
DR WPI; 2002-241737/29.
XX
PT Novel urocortin II polypeptide or human urocortin-related peptide, for
PT treating high body temperature, appetite dysfunction, congestive heart
PT failure, stress, anxiety and low levels of adrenocortico tropic hormone.
XX
PS Claim 2; Fig 4A; 94pp; English.
XX
CC The invention relates to a modified protein selected from urocortin II
CC (Ucn II) and human urocortin-related peptide (URP). A pharmaceutical
CC composition is useful for treating a pathophysiological state including
CC high body temperature, appetite dysfunction, congestive heart failure,
CC stress, anxiety and undesirably low levels of adrenocortico tropic
CC hormone (ACTH) secretions. A modified protein conjugate is useful in
CC scintigraphy and in various assays, and also for the targetted
CC destruction of Corticotropin-releasing factor (CRF) receptor bearing
CC cells. The present sequence is mouse urocortin II (ucn) protein
XX
SQ Sequence 112 AA;

Query Match 100.0%; Score 179; DB 5; Length 112;
Best Local Similarity 100.0%; Pred. No. 5.7e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
Db 72 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 109

RESULT 4
ADE64811
ID ADE64811 standard; peptide; 38 AA.
XX
AC ADE64811;
XX
DT 29-JAN-2004 (first entry)
XX
DE Corticotropin-releasing factor-2 polypeptide, SEQ ID No 114.
XX
KW corticotropin-releasing factor-2; CRF2; myopathic; osteopathic;
KW hypotensive; cardiant; vasotropic; antimigraine; cerebroprotective;
KW nootropic; neuroprotective; anorectic; antidiabetic; analgesic;
KW antiallergic; tranquilizer; anxiolytic; antidepressant; antiarthritic;
KW gene therapy.
XX
OS Unidentified.
XX

PN WO2003062277-A1.
XX
PD 31-JUL-2003.
XX
PF 16-JAN-2003; 2003WO-US001454.
XX
PR 16-JAN-2002; 2002US-0349117P.
PR 29-APR-2002; 2002US-0376337P.
PR 14-JUN-2002; 2002US-0388895P.
PR 19-SEP-2002; 2002US-0411988P.
XX
PA (PROC) PROCTER & GAMBLE CO.
XX
PI Isfort RJ, Mazur WA;
XX
DR WPI; 2003-787975/74.
XX
PT New non-native peptide derived from corticotropin-releasing factor-2,
PT useful for treatment and prevention of e.g. muscular atrophy, also
PT related nucleic acid and antibodies.
XX
PS Example 2; SEQ ID NO 114; 304pp; English.
XX
CC The invention relates to a novel non-native peptide derived from
CC corticotropin-releasing factor-2 (CRF2). The CRF2 peptides have the
CC following activities: myopathic, osteopathic, hypotensive, cardiant,
CC vasotropic, antimigraine, cerebroprotective, nootropic, neuroprotective,
CC anorectic, antidiabetic, analgesic, antiallergic, tranquilizer,
CC anxiolytic, antidepressant, and antiarthritic. The CRF2 peptides, and
CC related compounds derived from other proteins, are used to prevent or
CC treat disorders modulated by the CRF2 receptor, e.g. skeletal muscle
CC atrophy or wasting, and bone disorders, however caused; heart/circulatory
CC diseases (e.g. hypertension, congestive heart failure, heart attack,
CC reperfusion injury, migraine, stroke, memory loss, Alzheimer's disease,
CC dementia); joint disorders (osteoarthritis or rheumatoid arthritis);
CC metabolic disease (obesity or diabetes); pain; allergy; stress; anxiety;
CC low levels of adrenocorticotrophic hormone; anorexia nervosa; depression;
CC also to reduce body temperature and to control appetite or cognitive
CC function. Nucleic acids, optionally labelled, that encode the CRF2
CC peptides are used as primers and probes for amplification, also for gene
CC synthesis and for recombinant production of CRF2 peptides, including use
CC in gene therapy. Antibodies specific for the CRF2 peptides are used to
CC evaluate expression of the CRF2 peptides after gene therapy. This
CC sequence represents a novel native CRF polypeptide of the invention.
XX
SQ Sequence 38 AA;

Query Match 78.2%; Score 140; DB 7; Length 38;
Best Local Similarity 76.3%; Pred. No. 3.3e-15;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
::|||||||||||:|||||||:|||||||:|||:|||
Db 1 IVLSLDVPIGLLQILLEQARQRAAREQATTNARILARV 38

RESULT 5
ADE51097
ID ADE51097 standard; peptide; 38 AA.
XX
AC ADE51097;
XX
DT 29-JAN-2004 (first entry)
XX
DE CRF2 non-native polypeptide, SEQ ID No 114.
XX
KW non-native; corticotropin-releasing factor-2; CRF2; myopathic;
KW osteopathic; hypotensive; cardiant; vasotropic; antimigraine;
KW cerebroprotective; nootropic; neuroprotective; anorectic; antidiabetic;
KW analgesic; antiallergic; tranquilizer; anxiolytic; antidepressant;
KW antiarthritic.
XX
OS Unidentified.

XX
PN WO2003062268-A2.
XX
PD 31-JUL-2003.
XX
PF 16-JAN-2003; 2003WO-US001451.
XX
PR 16-JAN-2002; 2002US-0349117P.
PR 29-APR-2002; 2002US-0376337P.
PR 14-JUN-2002; 2002US-0388895P.
PR 19-SEP-2002; 2002US-0411988P.
XX
PA (PROC) PROCTER & GAMBLE CO.
XX
PI Isfort RJ, Mazur WA;
XX
DR WPI; 2003-787974/74.
XX
PT New non-native peptide derived from corticotropin-releasing factor-2,
PT useful for treatment and prevention of e.g. muscular atrophy, also
PT related nucleic acid and antibodies.
XX
PS Example 2; SEQ ID NO 114; 300pp; English.
XX
CC The invention relates to a novel non-native peptide derived from
CC corticotropin-releasing factor-2 (CRF2). The non-native CRF2 peptides
CC have the following activities: myopathic, osteopathic, hypotensive,
CC cardiant, vasotropic, antimigraine, cerebroprotective, nootropic,
CC neuroprotective, anorectic, antidiabetic, analgesic, antiallergic,
CC tranquilizer, anxiolytic, antidepressant, and antiarthritic. The non-
CC native CRF2 peptides, and related compounds derived from other proteins,
CC are used to prevent or treat disorders modulated by the CRF2 receptor,
CC e.g. skeletal muscle atrophy or wasting, and bone disorders, however
CC caused; heart/circulatory diseases (e.g. hypertension, congestive heart
CC failure, heart attack, reperfusion injury, migraine, stroke, memory loss,
CC Alzheimer's diseases, dementia); joint disorders (osteoarthritis or
CC rheumatoid arthritis); metabolic disease (obesity or diabetes); pain;
CC allergy; stress; anxiety; low levels of adrenocorticotrophic hormone;
CC anorexia nervosa; depression; also to reduce body temperature and to
CC control appetite or cognitive function. Nucleic acids, optionally
CC labelled, that encode the non-native CRF2 peptides are used as primers
CC and probes for amplification, also for gene synthesis and for recombinant
CC production of the non-native CRF2 peptides, including use in gene
CC therapy. Antibodies specific for the non-native CRF2 peptides are used to
CC evaluate expression of the non-native CRF2 peptides after gene therapy.
CC This sequence represents a CRF2 non-native polypeptide of the invention.
XX
SQ Sequence 38 AA;

Query Match 78.2%; Score 140; DB 7; Length 38;
Best Local Similarity 76.3%; Pred. No. 3.3e-15;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
::|||||||||||:|||||||:|||||||:|||:|||
Db 1 IVLSLDVPIGLLQILLEQARQRAAREQATTNARILARV 38

RESULT 6
AAE21009
ID AAE21009 standard; peptide; 38 AA.
XX
AC AAE21009;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human urocortin-related peptide (URP).
XX
KW Human; urocortin-related peptide; URP; antipyretic; cardiant; urocortin;
KW ucn; tranquilliser; appetite dysfunction; congestive heart failure;
KW stress; anxiety.
XX
OS Homo sapiens.

```
XX
FH   Key             Location/Qualifiers
FT   Modified-site   38
FT                   /note= "C-terminal amide"
XX
PN   WO200212307-A1.
XX
PD   14-FEB-2002.
XX
PF   31-JUL-2001; 2001WO-US023976.
XX
PR   04-AUG-2000; 2000US-0223255P.
PR   07-MAR-2001; 2001US-0273969P.
XX
PA   (RERE-) RES DEV FOUND.
XX
PI   Vale WW,  Sawchenko PF,  Lewis KA,  Vaughan JM,  Reyes TM,  Rivier JE;
PI   Hogenesch JB,  Perrin MH;
XX
DR   WPI; 2002-241737/29.
XX
PT   Novel urocortin II polypeptide or human urocortin-related peptide, for
PT   treating high body temperature, appetite dysfunction, congestive heart
PT   failure, stress, anxiety and low levels of adrenocortico tropic hormone.
XX
PS   Claim 36; Fig 4b; 94pp; English.
XX
CC   The invention relates to a modified protein selected from urocortin II
CC   (Ucn II) and human urocortin-related peptide (URP). A pharmaceutical
CC   composition is useful for treating a pathophysiological state including
CC   high body temperature, appetite dysfunction, congestive heart failure,
CC   stress, anxiety and undesirably low levels of adrenocortico tropic
CC   hormone (ACTH) secretions. A modified protein conjugate is useful in
CC   scintigraphy and in various assays, and also for the targetted
CC   destruction of Corticotropin-releasing factor (CRF) receptor bearing
CC   cells. The present sequence is human URP
XX
SQ   Sequence 38 AA;

  Query Match             77.7%;  Score 139;  DB 5;  Length 38;
  Best Local Similarity   76.3%;  Pred. No. 4.8e-15;
  Matches   29;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              ::||||||||||:|||||| :||| || |||:||| |
Db          1 IVLSLDVPIGLLQILLEQARARAAREQATTNARILARV 38


RESULT 7
AAO19442
ID   AAO19442 standard; peptide; 38 AA.
XX
AC   AAO19442;
XX
DT   10-DEC-2002  (first entry)
XX
DE   Human urocortin-related peptide.
XX
KW   Human; rat; mouse; sheep; cow; chicken; CRF1R; CRF2R;
KW   skeletal muscle atrophy; corticotrophin releasing factor-2 receptor;
KW   muscular dystrophy; corticotrophin releasing factor-1 receptor;
KW   gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200269908-A2.
XX
PD   12-SEP-2002.
XX
PF   06-MAR-2002; 2002WO-US007476.
XX
PR   06-MAR-2001; 2001US-00799978.
XX
PA   (PROC ) PROCTER & GAMBLE CO.
XX
PI   Isfort RJ,  Sheldon RJ;
XX
DR   WPI; 2002-713413/77.
XX
PT   Identifying candidate compounds for regulating skeletal muscle mass or
PT   treating skeletal muscle atrophy by identifying test compounds that bind
PT   to, or activate, the corticotropin releasing factor-2 receptor.
XX
PS   Disclosure; Page 164; 167pp; English.
XX
CC   The present invention relates to a method of identifying candidate
CC   compounds for regulating skeletal muscle mass or function, and comprises
CC   contacting a test compound with a corticotropin releasing factor-2
CC   receptor (CRF2R) or with a cell expressing a functional CRF2R,
CC   determining whether the test compound binds to, or activates, the CRF2R
CC   and identifying the test compounds that bind to, or activates, the CRF2R
CC   as candidate compounds for regulating skeletal muscle mass or function.
CC   The method is useful for preparing a medicament for treating skeletal
CC   muscle atrophy or for prophylactic treatment of muscular dystrophies. The
CC   present sequence is a human peptide shown in the invention
XX
SQ   Sequence 38 AA;

  Query Match             77.7%;  Score 139;  DB 5;  Length 38;
  Best Local Similarity   76.3%;  Pred. No. 4.8e-15;
  Matches   29;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              ::||||||||||:|||||| :||| || |||:||| |
Db          1 IVLSLDVPIGLLQILLEQARARAAREQATTNARILARV 38


RESULT 8
ABB82356
ID   ABB82356 standard; protein; 38 AA.
XX
AC   ABB82356;
XX
DT   08-JAN-2003  (first entry)
XX
DE   Human urocortin II protein (URP) fragment.
XX
KW   Urocortin III; Ucn-III; cardiant; antidiabetic; antimigraine; human;
KW   tranquilliser; antipyretic; vasotropic; gastrointestinal; antiangiogenic;
KW   vaccine; urocortin II; URP.
XX
OS   Homo sapiens.
XX
PN   WO200274326-A2.
XX
PD   26-SEP-2002.
XX
PF   15-MAR-2002; 2002WO-US009115.
XX
PR   15-MAR-2001; 2001US-0276069P.
PR   31-MAY-2001; 2001US-0294914P.
XX
PA   (RERE-) RES DEV FOUND.
XX
PI   Vale WW,  Rivier JE,  Kunitake KS,  Lewis KA,  Perrin MH,  Gulyas J;
XX
DR   WPI; 2002-740838/80.
XX
PT   New human or mouse urocortin III protein, useful e.g. for treating
PT   congestive heart failure, vascular disease, gastrointestinal dysfunction,
PT   diabetes mellitus, high temperature, appetite dysfunction and stress.
XX
PS   Example; Fig 2C; 81pp; English.
XX
CC   The invention relates to an isolated and purified human or mouse
CC   urocortin III (Ucn-III) protein. The Ucn-III protein is is useful: (i)
```

CC for treating a pathophysiological state including congestive heart
CC failure, vascular disease, gastrointestinal dysfunction, diabetes
CC mellitus, high temperature, appetite dysfunction, stress, undesirably low
CC levels of glucagon secretion or activity, anxiety and migraine headaches;
CC (ii) for determining whether a cell has urocortin III receptors; and
CC (iii) for inhibiting angiogenesis. The present sequence represents the
CC human urocortin II protein fragment
XX
SQ Sequence 38 AA;

Query Match 77.7%; Score 139; DB 5; Length 38;
Best Local Similarity 76.3%; Pred. No. 4.8e-15;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
::|||||||||||:|||||||:|||||||:|||:|||:|||||
Db 1 IVLSLDVPIGLLQILLEQARARAAREQATTNARILARV 38

RESULT 9
ADE64820
ID ADE64820 standard; peptide; 38 AA.
XX
AC ADE64820;
XX
DT 29-JAN-2004 (first entry)
XX
DE Corticotropin-releasing factor-2 polypeptide, SEQ ID No 123.
XX
KW corticotropin-releasing factor-2; CRF2; myopathic; osteopathic;
KW hypotensive; cardiant; vasotropic; antimigraine; cerebroprotective;
KW nootropic; neuroprotective; anorectic; antidiabetic; analgesic;
KW antiallergic; tranquilizer; anxiolytic; antidepressant; antiarthritic;
KW gene therapy.
XX
OS Unidentified.
XX
PN WO2003062277-A1.
XX
PD 31-JUL-2003.
XX
PF 16-JAN-2003; 2003WO-US001454.
XX
PR 16-JAN-2002; 2002US-0349117P.
PR 29-APR-2002; 2002US-0376337P.
PR 14-JUN-2002; 2002US-0388895P.
PR 19-SEP-2002; 2002US-0411988P.
XX
PA (PROC) PROCTER & GAMBLE CO.
XX
PI Isfort RJ, Mazur WA;
XX
DR WPI; 2003-787975/74.
XX
PT New non-native peptide derived from corticotropin-releasing factor-2,
PT useful for treatment and prevention of e.g. muscular atrophy, also
PT related nucleic acid and antibodies.
XX
PS Example 2; SEQ ID NO 123; 304pp; English.
XX
CC The invention relates to a novel non-native peptide derived from
CC corticotropin-releasing factor-2 (CRF2). The CRF2 peptides have the
CC following activities: myopathic, osteopathic, hypotensive, cardiant,
CC vasotropic, antimigraine, cerebroprotective, nootropic, neuroprotective,
CC anorectic, antidiabetic, analgesic, antiallergic, tranquilizer,
CC anxiolytic, antidepressant, and antiarthritic. The CRF2 peptides, and
CC related compounds derived from other proteins, are used to prevent or
CC treat disorders modulated by the CRF2 receptor, e.g. skeletal muscle
CC atrophy or wasting, and bone disorders, however caused; heart/circulatory
CC diseases (e.g. hypertension, congestive heart failure, heart attack,
CC reperfusion injury, migraine, stroke, memory loss, Alzheimer's disease,
CC dementia); joint disorders (osteoarthritis or rheumatoid arthritis);
CC metabolic disease (obesity or diabetes); pain; allergy; stress; anxiety;
CC low levels of adrenocorticotrophic hormone; anorexia nervosa; depression;
CC also to reduce body temperature and to control appetite or cognitive
CC function. Nucleic acids, optionally labelled, that encode the CRF2
CC peptides are used as primers and probes for amplification, also for gene
CC synthesis and for recombinant production of CRF2 peptides, including use
CC in gene therapy. Antibodies specific for the CRF2 peptides are used to
CC evaluate expression of the CRF2 peptides after gene therapy. This
CC sequence represents a novel native CRF polypeptide of the invention.
XX
SQ Sequence 38 AA;

Query Match 77.7%; Score 139; DB 7; Length 38;
Best Local Similarity 76.3%; Pred. No. 4.8e-15;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
::|||||||||||:|||||||:|||||||:|||:|||:|||||
Db 1 IVLSLDVPIGLLQILLEQARQEAAREQATTNARILARV 38

RESULT 10
ADE64701
ID ADE64701 standard; peptide; 38 AA.
XX
AC ADE64701;
XX
DT 29-JAN-2004 (first entry)
XX
DE CRF-2 related human urocortin II polypeptide, SEQ ID No 4.
XX
KW corticotropin-releasing factor-2; CRF2; myopathic; osteopathic;
KW hypotensive; cardiant; vasotropic; antimigraine; cerebroprotective;
KW nootropic; neuroprotective; anorectic; antidiabetic; analgesic;
KW antiallergic; tranquilizer; anxiolytic; antidepressant; antiarthritic;
KW gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO2003062277-A1.
XX
PD 31-JUL-2003.
XX
PF 16-JAN-2003; 2003WO-US001454.
XX
PR 16-JAN-2002; 2002US-0349117P.
PR 29-APR-2002; 2002US-0376337P.
PR 14-JUN-2002; 2002US-0388895P.
PR 19-SEP-2002; 2002US-0411988P.
XX
PA (PROC) PROCTER & GAMBLE CO.
XX
PI Isfort RJ, Mazur WA;
XX
DR WPI; 2003-787975/74.
XX
PT New non-native peptide derived from corticotropin-releasing factor-2,
PT useful for treatment and prevention of e.g. muscular atrophy, also
PT related nucleic acid and antibodies.
XX
PS Example 1; SEQ ID NO 4; 304pp; English.
XX
CC The invention relates to a novel non-native peptide derived from
CC corticotropin-releasing factor-2 (CRF2). The CRF2 peptides have the
CC following activities: myopathic, osteopathic, hypotensive, cardiant,
CC vasotropic, antimigraine, cerebroprotective, nootropic, neuroprotective,
CC anorectic, antidiabetic, analgesic, antiallergic, tranquilizer,
CC anxiolytic, antidepressant, and antiarthritic. The CRF2 peptides, and
CC related compounds derived from other proteins, are used to prevent or
CC treat disorders modulated by the CRF2 receptor, e.g. skeletal muscle
CC atrophy or wasting, and bone disorders, however caused; heart/circulatory
CC diseases (e.g. hypertension, congestive heart failure, heart attack,
CC reperfusion injury, migraine, stroke, memory loss, Alzheimer's disease,
CC dementia); joint disorders (osteoarthritis or rheumatoid arthritis);

CC metabolic disease (obesity or diabetes); pain; allergy; stress; anxiety;
CC low levels of adrenocorticotrophic hormone; anorexia nervosa; depression;
CC also to reduce body temperature and to control appetite or cognitive
CC function. Nucleic acids, optionally labelled, that encode the CRF2
CC peptides are used as primers and probes for amplification, also for gene
CC synthesis and for recombinant production of CRF2 peptides, including use
CC in gene therapy. Antibodies specific for the CRF2 peptides are used to
CC evaluate expression of the CRF2 peptides after gene therapy. This
CC sequence represents a novel native CRF polypeptide of the invention.
XX
SQ Sequence 38 AA;

Query Match 77.7%; Score 139; DB 7; Length 38;
Best Local Similarity 76.3%; Pred. No. 4.8e-15;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
::|||||||||||:|||||||:|||||||:|||:|
Db 1 IVLSLDVPIGLLQILLEQARARAAREQATTNARILARV 38

RESULT 11
ADE65051
ID ADE65051 standard; peptide; 38 AA.
XX
AC ADE65051;
XX
DT 29-JAN-2004 (first entry)
XX
DE Corticotropin-releasing factor-2 polypeptide, SEQ ID No 354.
XX
KW corticotropin-releasing factor-2; CRF2; myopathic; osteopathic;
KW hypotensive; cardiant; vasotropic; antimigraine; cerebroprotective;
KW nootropic; neuroprotective; anorectic; antidiabetic; analgesic;
KW antiallergic; tranquilizer; anxiolytic; antidepressant; antiarthritic;
KW gene therapy.
XX
OS Unidentified.
XX
PN WO2003062277-A1.
XX
PD 31-JUL-2003.
XX
PF 16-JAN-2003; 2003WO-US001454.
XX
PR 16-JAN-2002; 2002US-0349117P.
PR 29-APR-2002; 2002US-0376337P.
PR 14-JUN-2002; 2002US-0388895P.
PR 19-SEP-2002; 2002US-0411988P.
XX
PA (PROC) PROCTER & GAMBLE CO.
XX
PI Isfort RJ, Mazur WA;
XX
DR WPI; 2003-787975/74.
XX
PT New non-native peptide derived from corticotropin-releasing factor-2,
PT useful for treatment and prevention of e.g. muscular atrophy, also
PT related nucleic acid and antibodies.
XX
PS Example 2; SEQ ID NO 354; 304pp; English.
XX
CC The invention relates to a novel non-native peptide derived from
CC corticotropin-releasing factor-2 (CRF2). The CRF2 peptides have the
CC following activities: myopathic, osteopathic, hypotensive, cardiant,
CC vasotropic, antimigraine, cerebroprotective, nootropic, neuroprotective,
CC anorectic, antidiabetic, analgesic, antiallergic, tranquilizer,
CC anxiolytic, antidepressant, and antiarthritic. The CRF2 peptides, and
CC related compounds derived from other proteins, are used to prevent or
CC treat disorders modulated by the CRF2 receptor, e.g. skeletal muscle
CC atrophy or wasting, and bone disorders, however caused; heart/circulatory
CC diseases (e.g. hypertension, congestive heart failure, heart attack,
CC reperfusion injury, migraine, stroke, memory loss, Alzheimer's disease,
CC dementia); joint disorders (osteoarthritis or rheumatoid arthritis);
CC metabolic disease (obesity or diabetes); pain; allergy; stress; anxiety;
CC low levels of adrenocorticotrophic hormone; anorexia nervosa; depression;
CC also to reduce body temperature and to control appetite or cognitive
CC function. Nucleic acids, optionally labelled, that encode the CRF2
CC peptides are used as primers and probes for amplification, also for gene
CC synthesis and for recombinant production of CRF2 peptides, including use
CC in gene therapy. Antibodies specific for the CRF2 peptides are used to
CC evaluate expression of the CRF2 peptides after gene therapy. This
CC sequence represents a novel native CRF polypeptide of the invention.
XX
SQ Sequence 38 AA;

Query Match 77.7%; Score 139; DB 7; Length 38;
Best Local Similarity 76.3%; Pred. No. 4.8e-15;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
::|||||||||||:|||||||:|||||||:|||:|
Db 1 IVLSLDVPIGLLQILLEQARARAAREQATTNARILARV 38

RESULT 12
ADE51106
ID ADE51106 standard; peptide; 38 AA.
XX
AC ADE51106;
XX
DT 29-JAN-2004 (first entry)
XX
DE CRF2 non-native polypeptide, SEQ ID No 123.
XX
KW non-native; corticotropin-releasing factor-2; CRF2; myopathic;
KW osteopathic; hypotensive; cardiant; vasotropic; antimigraine;
KW cerebroprotective; nootropic; neuroprotective; anorectic; antidiabetic;
KW analgesic; antiallergic; tranquilizer; anxiolytic; antidepressant;
KW antiarthritic.
XX
OS Unidentified.
XX
PN WO2003062268-A2.
XX
PD 31-JUL-2003.
XX
PF 16-JAN-2003; 2003WO-US001451.
XX
PR 16-JAN-2002; 2002US-0349117P.
PR 29-APR-2002; 2002US-0376337P.
PR 14-JUN-2002; 2002US-0388895P.
PR 19-SEP-2002; 2002US-0411988P.
XX
PA (PROC) PROCTER & GAMBLE CO.
XX
PI Isfort RJ, Mazur WA;
XX
DR WPI; 2003-787974/74.
XX
PT New non-native peptide derived from corticotropin-releasing factor-2,
PT useful for treatment and prevention of e.g. muscular atrophy, also
PT related nucleic acid and antibodies.
XX
PS Example 2; SEQ ID NO 123; 300pp; English.
XX
CC The invention relates to a novel non-native peptide derived from
CC corticotropin-releasing factor-2 (CRF2). The non-native CRF2 peptides
CC have the following activities: myopathic, osteopathic, hypotensive,
CC cardiant, vasotropic, antimigraine, cerebroprotective, nootropic,
CC neuroprotective, anorectic, antidiabetic, analgesic, antiallergic,
CC tranquilizer, anxiolytic, antidepressant, and antiarthritic. The non-
CC native CRF2 peptides, and related compounds derived from other proteins,
CC are used to prevent or treat disorders modulated by the CRF2 receptor,
CC e.g. skeletal muscle atrophy or wasting, and bone disorders, however
CC caused; heart/circulatory diseases (e.g. hypertension, congestive heart

CC failure, heart attack, reperfusion injury, migraine, stroke, memory loss,
CC Alzheimer's diseases, dementia); joint disorders (osteoarthritis or
CC rheumatoid arthritis); metabolic disease (obesity or diabetes); pain;
CC allergy; stress; anxiety; low levels of adrenocorticotrophic hormone;
CC anorexia nervosa; depression; also to reduce body temperature and to
CC control appetite or cognitive function. Nucleic acids, optionally
CC labelled, that encode the non-native CRF2 peptides are used as primers
CC and probes for amplification, also for gene synthesis and for recombinant
CC production of the non-native CRF2 peptides, including use in gene
CC therapy. Antibodies specific for the non-native CRF2 peptides are used to
CC evaluate expression of the non-native CRF2 peptides after gene therapy.
CC This sequence represents a CRF2 non-native polypeptide of the invention.
XX
SQ Sequence 38 AA;

Query Match 77.7%; Score 139; DB 7; Length 38;
Best Local Similarity 76.3%; Pred. No. 4.8e-15;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
::|||||||||||:|||||||:|||||||:|||:|||
Db 1 IVLSLDVPIGLLQILLEQARQEAAREQATTNARILARV 38

RESULT 13
ADE51337
ID ADE51337 standard; peptide; 38 AA.
XX
AC ADE51337;
XX
DT 29-JAN-2004 (first entry)
XX
DE CRF2 non-native polypeptide, SEQ ID No 354.
XX
KW non-native; corticotropin-releasing factor-2; CRF2; myopathic;
KW osteopathic; hypotensive; cardiant; vasotropic; antimigraine;
KW cerebroprotective; nootropic; neuroprotective; anorectic; antidiabetic;
KW analgesic; antiallergic; tranquilizer; anxiolytic; antidepressant;
KW antiarthritic.
XX
OS Unidentified.
XX
PN WO2003062268-A2.
XX
PD 31-JUL-2003.
XX
PF 16-JAN-2003; 2003WO-US001451.
XX
PR 16-JAN-2002; 2002US-0349117P.
PR 29-APR-2002; 2002US-0376337P.
PR 14-JUN-2002; 2002US-0388895P.
PR 19-SEP-2002; 2002US-0411988P.
XX
PA (PROC) PROCTER & GAMBLE CO.
XX
PI Isfort RJ, Mazur WA;
XX
DR WPI; 2003-787974/74.
XX
PT New non-native peptide derived from corticotropin-releasing factor-2,
PT useful for treatment and prevention of e.g. muscular atrophy, also
PT related nucleic acid and antibodies.
XX
PS Example 2; SEQ ID NO 354; 300pp; English.
XX
CC The invention relates to a novel non-native peptide derived from
CC corticotropin-releasing factor-2 (CRF2). The non-native CRF2 peptides
CC have the following activities: myopathic, osteopathic, hypotensive,
CC cardiant, vasotropic, antimigraine, cerebroprotective, nootropic,
CC neuroprotective, anorectic, antidiabetic, analgesic, antiallergic,
CC tranquilizer, anxiolytic, antidepressant, and antiarthritic. The non-
CC native CRF2 peptides, and related compounds derived from other proteins,
CC are used to prevent or treat disorders modulated by the CRF2 receptor,
CC e.g. skeletal muscle atrophy or wasting, and bone disorders, however
CC caused; heart/circulatory diseases (e.g. hypertension, congestive heart
CC failure, heart attack, reperfusion injury, migraine, stroke, memory loss,
CC Alzheimer's diseases, dementia); joint disorders (osteoarthritis or
CC rheumatoid arthritis); metabolic disease (obesity or diabetes); pain;
CC allergy; stress; anxiety; low levels of adrenocorticotrophic hormone;
CC anorexia nervosa; depression; also to reduce body temperature and to
CC control appetite or cognitive function. Nucleic acids, optionally
CC labelled, that encode the non-native CRF2 peptides are used as primers
CC and probes for amplification, also for gene synthesis and for recombinant
CC production of the non-native CRF2 peptides, including use in gene
CC therapy. Antibodies specific for the non-native CRF2 peptides are used to
CC evaluate expression of the non-native CRF2 peptides after gene therapy.
CC This sequence represents a CRF2 non-native polypeptide of the invention.
XX
SQ Sequence 38 AA;

Query Match 77.7%; Score 139; DB 7; Length 38;
Best Local Similarity 76.3%; Pred. No. 4.8e-15;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
::|||||||||||:|||||||:|||||||:|||:|||
Db 1 IVLSLDVPIGLLQILLEQARARAAREQATTNARILARV 38

RESULT 14
ADE50987
ID ADE50987 standard; peptide; 38 AA.
XX
AC ADE50987;
XX
DT 29-JAN-2004 (first entry)
XX
DE CRF2 human urocortin II native polypeptide, SEQ ID No 4.
XX
KW non-native; corticotropin-releasing factor-2; CRF2; myopathic;
KW osteopathic; hypotensive; cardiant; vasotropic; antimigraine;
KW cerebroprotective; nootropic; neuroprotective; anorectic; antidiabetic;
KW analgesic; antiallergic; tranquilizer; anxiolytic; antidepressant;
KW antiarthritic; human.
XX
OS Homo sapiens.
XX
PN WO2003062268-A2.
XX
PD 31-JUL-2003.
XX
PF 16-JAN-2003; 2003WO-US001451.
XX
PR 16-JAN-2002; 2002US-0349117P.
PR 29-APR-2002; 2002US-0376337P.
PR 14-JUN-2002; 2002US-0388895P.
PR 19-SEP-2002; 2002US-0411988P.
XX
PA (PROC) PROCTER & GAMBLE CO.
XX
PI Isfort RJ, Mazur WA;
XX
DR WPI; 2003-787974/74.
XX
PT New non-native peptide derived from corticotropin-releasing factor-2,
PT useful for treatment and prevention of e.g. muscular atrophy, also
PT related nucleic acid and antibodies.
XX
PS Example 1; SEQ ID NO 4; 300pp; English.
XX
CC The invention relates to a novel non-native peptide derived from
CC corticotropin-releasing factor-2 (CRF2). The non-native CRF2 peptides
CC have the following activities: myopathic, osteopathic, hypotensive,
CC cardiant, vasotropic, antimigraine, cerebroprotective, nootropic,
CC neuroprotective, anorectic, antidiabetic, analgesic, antiallergic,
CC tranquilizer, anxiolytic, antidepressant, and antiarthritic. The non-

CC native CRF2 peptides, and related compounds derived from other proteins,
CC are used to prevent or treat disorders modulated by the CRF2 receptor,
CC e.g. skeletal muscle atrophy or wasting, and bone disorders, however
CC caused; heart/circulatory diseases (e.g. hypertension, congestive heart
CC failure, heart attack, reperfusion injury, migraine, stroke, memory loss,
CC Alzheimer's diseases, dementia); joint disorders (osteoarthritis or
CC rheumatoid arthritis); metabolic disease (obesity or diabetes); pain;
CC allergy; stress; anxiety; low levels of adrenocorticotrophic hormone;
CC anorexia nervosa; depression; also to reduce body temperature and to
CC control appetite or cognitive function. Nucleic acids, optionally
CC labelled, that encode the non-native CRF2 peptides are used as primers
CC and probes for amplification, also for gene synthesis and for recombinant
CC production of the non-native CRF2 peptides, including use in gene
CC therapy. Antibodies specific for the non-native CRF2 peptides are used to
CC evaluate expression of the non-native CRF2 peptides after gene therapy.
CC This sequence represents a human urocortin II native polypeptide relating
CC to the CRF2 non-native polypeptides of the invention.
XX
SQ Sequence 38 AA;

Query Match 77.7%; Score 139; DB 7; Length 38;
Best Local Similarity 76.3%; Pred. No. 4.8e-15;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              ::|||||||||||:|||||||  :|||  ||  |||:|||  |
Db          1 IVLSLDVPIGLLQILLEQARARAAREQATTNARILARV 38
```

RESULT 15
ADE65065
ID ADE65065 standard; peptide; 39 AA.
XX
AC ADE65065;
XX
DT 29-JAN-2004 (first entry)
XX
DE Corticotropin-releasing factor-2 polypeptide, SEQ ID No 368.
XX
KW corticotropin-releasing factor-2; CRF2; myopathic; osteopathic;
KW hypotensive; cardiant; vasotropic; antimigraine; cerebroprotective;
KW nootropic; neuroprotective; anorectic; antidiabetic; analgesic;
KW antiallergic; tranquilizer; anxiolytic; antidepressant; antiarthritic;
KW gene therapy.
XX
OS Unidentified.
XX
PN WO2003062277-A1.
XX
PD 31-JUL-2003.
XX
PF 16-JAN-2003; 2003WO-US001454.
XX
PR 16-JAN-2002; 2002US-0349117P.
PR 29-APR-2002; 2002US-0376337P.
PR 14-JUN-2002; 2002US-0388895P.
PR 19-SEP-2002; 2002US-0411988P.
XX
PA (PROC) PROCTER & GAMBLE CO.
XX
PI Isfort RJ, Mazur WA;
XX
DR WPI; 2003-787975/74.
XX
PT New non-native peptide derived from corticotropin-releasing factor-2,
PT useful for treatment and prevention of e.g. muscular atrophy, also
PT related nucleic acid and antibodies.
XX
PS Example 2; SEQ ID NO 368; 304pp; English.
XX
CC The invention relates to a novel non-native peptide derived from
CC corticotropin-releasing factor-2 (CRF2). The CRF2 peptides have the
CC following activities: myopathic, osteopathic, hypotensive, cardiant,
CC vasotropic, antimigraine, cerebroprotective, nootropic, neuroprotective,
CC anorectic, antidiabetic, analgesic, antiallergic, tranquilizer,
CC anxiolytic, antidepressant, and antiarthritic. The CRF2 peptides, and
CC related compounds derived from other proteins, are used to prevent or
CC treat disorders modulated by the CRF2 receptor, e.g. skeletal muscle
CC atrophy or wasting, and bone disorders, however caused; heart/circulatory
CC diseases (e.g. hypertension, congestive heart failure, heart attack,
CC reperfusion injury, migraine, stroke, memory loss, Alzheimer's disease,
CC dementia); joint disorders (osteoarthritis or rheumatoid arthritis);
CC metabolic disease (obesity or diabetes); pain; allergy; stress; anxiety;
CC low levels of adrenocorticotrophic hormone; anorexia nervosa; depression;
CC also to reduce body temperature and to control appetite or cognitive
CC function. Nucleic acids, optionally labelled, that encode the CRF2
CC peptides are used as primers and probes for amplification, also for gene
CC synthesis and for recombinant production of CRF2 peptides, including use
CC in gene therapy. Antibodies specific for the CRF2 peptides are used to
CC evaluate expression of the CRF2 peptides after gene therapy. This
CC sequence represents a novel native CRF polypeptide of the invention.
XX
SQ Sequence 39 AA;

Query Match 77.7%; Score 139; DB 7; Length 39;
Best Local Similarity 76.3%; Pred. No. 5e-15;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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Qy          1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              ::|||||||||||:|||||||  :|||  ||  |||:|||  |
Db          1 IVLSLDVPIGLLQILLEQARARAAREQATTNARILARV 38
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Search completed: April 20, 2004, 18:54:43
Job time : 25.3333 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 20, 2004, 18:53:13 ; Search time 8.36 Seconds
(without alignments)
234.664 Million cell updates/sec

Title: US-09-919-473-11
Perfect score: 179
Sequence: 1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	179	100.0	38	4	US-09-799-978-43	Sequence 43, Appl
2	139	77.7	38	4	US-09-799-978-44	Sequence 44, Appl
3	63	35.2	41	4	US-09-260-846-25	Sequence 25, Appl
4	61	34.1	41	1	US-07-709-091-8	Sequence 8, Appli
5	61	34.1	41	1	US-08-104-862-8	Sequence 8, Appli
6	61	34.1	41	1	US-08-865-773-9	Sequence 9, Appli
7	61	34.1	41	3	US-08-981-189B-4	Sequence 4, Appli
8	61	34.1	41	4	US-09-400-716-6	Sequence 6, Appli
9	61	34.1	41	4	US-09-400-716-7	Sequence 7, Appli
10	61	34.1	41	4	US-09-424-127-9	Sequence 9, Appli
11	61	34.1	41	6	5177060-6	Patent No. 5177060
12	60	33.5	40	3	US-08-981-189B-8	Sequence 8, Appli
13	60	33.5	40	4	US-09-400-716-10	Sequence 10, Appl
14	60	33.5	40	4	US-09-400-716-11	Sequence 11, Appl
15	60	33.5	40	4	US-09-356-139-3	Sequence 3, Appli
16	60	33.5	41	1	US-08-865-773-8	Sequence 8, Appli
17	60	33.5	41	3	US-08-981-189B-5	Sequence 5, Appli
18	60	33.5	41	3	US-08-981-189B-17	Sequence 17, Appl
19	60	33.5	41	4	US-09-424-127-8	Sequence 8, Appli
20	60	33.5	41	6	5177060-7	Patent No. 5177060
21	60	33.5	124	3	US-08-981-189B-15	Sequence 15, Appl
22	58	32.4	41	1	US-07-709-091-3	Sequence 3, Appli
23	58	32.4	41	1	US-07-715-752A-3	Sequence 3, Appli
24	58	32.4	41	1	US-08-104-862-3	Sequence 3, Appli
25	58	32.4	41	1	US-08-162-178-3	Sequence 3, Appli
26	58	32.4	41	1	US-08-865-773-4	Sequence 4, Appli
27	58	32.4	41	4	US-09-424-127-4	Sequence 4, Appli
28	58	32.4	41	5	PCT-US92-05101-3	Sequence 3, Appli
29	57	31.8	41	1	US-07-709-091-2	Sequence 2, Appli
30	57	31.8	41	1	US-07-715-752A-2	Sequence 2, Appli
31	57	31.8	41	1	US-08-104-862-2	Sequence 2, Appli
32	57	31.8	41	1	US-08-162-178-2	Sequence 2, Appli
33	57	31.8	41	1	US-08-480-756-7	Sequence 7, Appli
34	57	31.8	41	1	US-08-865-773-2	Sequence 2, Appli
35	57	31.8	41	1	US-08-865-773-5	Sequence 5, Appli
36	57	31.8	41	3	US-08-888-381-3	Sequence 3, Appli
37	57	31.8	41	3	US-08-981-189B-3	Sequence 3, Appli
38	57	31.8	41	4	US-09-400-716-1	Sequence 1, Appli
39	57	31.8	41	4	US-09-400-716-2	Sequence 2, Appli
40	57	31.8	41	4	US-09-424-127-2	Sequence 2, Appli
41	57	31.8	41	4	US-09-424-127-5	Sequence 5, Appli
42	57	31.8	41	4	US-09-356-139-1	Sequence 1, Appli
43	57	31.8	41	5	PCT-US92-05101-2	Sequence 2, Appli
44	57	31.8	41	6	5177060-1	Patent No. 5177060
45	57	31.8	41	6	5177060-2	Patent No. 5177060

ALIGNMENTS

RESULT 1
US-09-799-978-43
; Sequence 43, Application US/09799978
; Patent No. 6670140
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert
; APPLICANT: Sheldon, Russell
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or
; TITLE OF INVENTION: Function Using Corticotropin Releasing Factor Receptors
; FILE REFERENCE: 8448
; CURRENT APPLICATION NUMBER: US/09/799,978
; CURRENT FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-799-978-43

Query Match 100.0%; Score 179; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 3.2e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              |||||||||||||||||||||||||||||||||||||||
Db          1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
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RESULT 2
US-09-799-978-44
; Sequence 44, Application US/09799978
; Patent No. 6670140
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert
; APPLICANT: Sheldon, Russell
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or
; TITLE OF INVENTION: Function Using Corticotropin Releasing Factor Receptors
; FILE REFERENCE: 8448
; CURRENT APPLICATION NUMBER: US/09/799,978
; CURRENT FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-978-44

```
  Query Match             77.7%;  Score 139;  DB 4;  Length 38;
  Best Local Similarity   76.3%;  Pred. No. 6.3e-15;
  Matches   29;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              ::|||||||||:|||||| :||| || |||:||| |
Db          1 IVLSLDVPIGLLQILLEQARARAAREQATTNARILARV 38


RESULT 3
US-09-260-846-25
; Sequence 25, Application US/09260846
; Patent No. 6307017
; GENERAL INFORMATION:
;  APPLICANT: Coy, David H.
;  APPLICANT: Moreau, Jacques-Pierre
;  APPLICANT: Kim, Sun Hyuk
;  TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN ANALOGS
;  FILE REFERENCE: 00537/00900J
;  CURRENT APPLICATION NUMBER: US/09/260,846
;  CURRENT FILING DATE: 1999-03-02
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
;   LENGTH: 41
;   TYPE: PRT
;   ORGANISM: mammalian
;   FEATURE:
;   OTHER INFORMATION: Homo sapiens/Porcine/Bovine
;   FEATURE:
;   OTHER INFORMATION: this peptide has an amidated c-terminus
US-09-260-846-25

  Query Match             35.2%;  Score 63;  DB 4;  Length 41;
  Best Local Similarity   41.7%;  Pred. No. 0.0062;
  Matches   15;  Conservative    6;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              :|||:   ||| ::| || :  | ||  | : | |
Db          6 ISLDLTFHLLRNMIEMARIENEREQAGLNRKYLDEV 41


RESULT 4
US-07-709-091-8
; Sequence 8, Application US/07709091
; Patent No. 5235036
;  GENERAL INFORMATION:
;    APPLICANT:  Kornreich, Wayne D
;    APPLICANT:  Hernandez, Jean-Francois
;    APPLICANT:  Rivier, Jean E F
;    APPLICANT:  Vale Jr, Wylie W
;    TITLE OF INVENTION:  CRF Analogs
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fitch, Even, Tabin & Flannery
;      STREET:  135 South LaSalle Street, Suite 900
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/709,091
;      FILING DATE:  19910531
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Schumann, James J
;      REGISTRATION NUMBER:  20856
;      REFERENCE/DOCKET NUMBER:  51339
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619)552-1311
;      TELEFAX:  (619)552-0095
;      TELEX:  20 6566 PATLAW CGO
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  41 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-07-709-091-8

  Query Match             34.1%;  Score 61;  DB 1;  Length 41;
  Best Local Similarity   41.2%;  Pred. No. 0.013;
  Matches   14;  Conservative    8;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQILA 36
              :|||:   ||| :|| || :    || :| :::|
Db          6 ISLDLTFHLLREVLEMARAEQLAQQAHSNRKLMA 39


RESULT 5
US-08-104-862-8
; Sequence 8, Application US/08104862
; Patent No. 5439885
;  GENERAL INFORMATION:
;    APPLICANT:  Kornreich, Wayne D
;    APPLICANT:  Hernandez, Jean-Francois
;    APPLICANT:  Rivier, Jean E F
;    APPLICANT:  Vale Jr, Wylie W
;    TITLE OF INVENTION:  CRF Analogs
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fitch, Even, Tabin & Flannery
;      STREET:  135 South LaSalle Street, Suite 900
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/104,862
;      FILING DATE:  19930810
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/709,091
;      FILING DATE:  31-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Schumann, J. J.
;      REGISTRATION NUMBER:  20,856
;      REFERENCE/DOCKET NUMBER:  54538
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-552-1311
;      TELEFAX:  619-552-0095
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  41 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-08-104-862-8

  Query Match             34.1%;  Score 61;  DB 1;  Length 41;
  Best Local Similarity   41.2%;  Pred. No. 0.013;
  Matches   14;  Conservative    8;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQILA 36
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Db          6 ISLDLTFHLLREVLEMARAEQLAQQAHSNRKLMA 39


RESULT 6
US-08-865-773-9
; Sequence 9, Application US/08865773
; Patent No. 5777073
;  GENERAL INFORMATION:
;    APPLICANT:  RIVIER, Jean E.F.
;    TITLE OF INVENTION:  CYCLIC CRF ANTAGONIST PEPTIDES
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FITCH, EVEN, TABIN & FLANNERY
;      STREET:  135 S. LaSalle Street, Suite 900
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/865,773
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/556,578
;      FILING DATE:  13-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/353,928
;      FILING DATE:  12-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Schumann, James J.
;      REGISTRATION NUMBER:  20,856
;      REFERENCE/DOCKET NUMBER:  57670
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-552-1311
;      TELEFAX:  619-552-0095
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  41 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-865-773-9

  Query Match             34.1%;  Score 61;  DB 1;  Length 41;
  Best Local Similarity   38.9%;  Pred. No. 0.013;
  Matches   14;  Conservative    7;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              :|:|:   ||| ::| || :  | ||  | : |  |
Db          6 ISIDLTFHLLRNMIEMARIENEREQAGLNRKYLDEV 41


RESULT 7
US-08-981-189B-4
; Sequence 4, Application US/08981189B
; Patent No. 6214797
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  UROCORTIN PEPTIDES
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FITCH, EVEN, TABIN & FLANNERY
;      STREET:  120 S. LaSalle Street, Suite 1600
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/981,189B
;      FILING DATE:  10-DEC-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/028,144
;      FILING DATE:  13-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/002,223
;      FILING DATE:  11-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Schumann, James J.
;      REGISTRATION NUMBER:  20,856
;      REFERENCE/DOCKET NUMBER:  57611
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  858-552-1311
;      TELEFAX:  858-552-0095
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  41 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-981-189B-4

  Query Match             34.1%;  Score 61;  DB 3;  Length 41;
  Best Local Similarity   38.9%;  Pred. No. 0.013;
  Matches   14;  Conservative    7;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              :|:|:   ||| ::| || :  | ||  | : |  |
Db          6 ISIDLTFHLLRNMIEMARIENEREQAGLNRKYLDEV 41


RESULT 8
US-09-400-716-6
; Sequence 6, Application US/09400716
; Patent No. 6319900
; GENERAL INFORMATION:
;  APPLICANT:  Wei, Edward T.
;  APPLICANT:  Slominski, Andrzej T.
;  TITLE OF INVENTION:  INHIBITION OF ABNORMAL CELL GROWTH WITH
;  TITLE OF INVENTION:  CORTICOTROPIN-RELEASING HORMONE ANALOGS
;  FILE REFERENCE:  2900.006US0
;  CURRENT APPLICATION NUMBER: US/09/400,716
;  CURRENT FILING DATE:  1999-09-21
;  NUMBER OF SEQ ID NOS:  12
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 41
;   TYPE: PRT
;   ORGANISM: Sucker fish
US-09-400-716-6

  Query Match             34.1%;  Score 61;  DB 4;  Length 41;
  Best Local Similarity   38.9%;  Pred. No. 0.013;
  Matches   14;  Conservative    7;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              :|:|:   ||| ::| || :  | ||  | : |  |
Db          6 ISIDLTFHLLRNMIEMARIENEREQAGLNRKYLDEV 41


RESULT 9
US-09-400-716-7
; Sequence 7, Application US/09400716
; Patent No. 6319900
; GENERAL INFORMATION:
;  APPLICANT:  Wei, Edward T.
;  APPLICANT:  Slominski, Andrzej T.
;  TITLE OF INVENTION:  INHIBITION OF ABNORMAL CELL GROWTH WITH
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;  TITLE OF INVENTION:  CORTICOTROPIN-RELEASING HORMONE ANALOGS
;  FILE REFERENCE:  2900.006US0
;  CURRENT APPLICATION NUMBER: US/09/400,716
;  CURRENT FILING DATE:  1999-09-21
;  NUMBER OF SEQ ID NOS:  12
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 41
;   TYPE: PRT
;   ORGANISM: Carp
US-09-400-716-7

  Query Match             34.1%;  Score 61;  DB 4;  Length 41;
  Best Local Similarity   38.9%;  Pred. No. 0.013;
  Matches   14;  Conservative    7;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              :|:|:   ||| ::| || :  | ||  | : |  |
Db          6 ISIDLTFHLLRNMIEMARIENEREQAGLNRKYLDEV 41


RESULT 10
US-09-424-127-9
; Sequence 9, Application US/09424127
; Patent No. 6323312
;   GENERAL INFORMATION:
;        APPLICANT: RIVIER, Jean E.F.
;        TITLE OF INVENTION: CYCLIC CRF ANTAGONIST PEPTIDES
;        NUMBER OF SEQUENCES: 11
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: FITCH, EVEN, TABIN & FLANNERY
;             STREET: 135 S. LaSalle Street, Suite 900
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60603
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/424,127
;             FILING DATE: 17-No. 6323312-1999
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/865,773
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Schumann, James J.
;             REGISTRATION NUMBER: 20,856
;             REFERENCE/DOCKET NUMBER: 57670
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 619-552-1311
;             TELEFAX: 619-552-0095
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 41 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-424-127-9

  Query Match             34.1%;  Score 61;  DB 4;  Length 41;
  Best Local Similarity   38.9%;  Pred. No. 0.013;
  Matches   14;  Conservative    7;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              :|:|:   ||| ::| || :  | ||  | : |  |
Db          6 ISIDLTFHLLRNMIEMARIENEREQAGLNRKYLDEV 41


RESULT 11
5177060-6
;Patent No. 5177060
;    APPLICANT: WEI, EDWARD T.
;    TITLE OF INVENTION: ANTI-INFLAMMATORY PEPTIDES AND TREATMENT
;TO INHIBIT VASCULAR LEAKAGE IN INJURED TISSUES
;    NUMBER OF SEQUENCES: 30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/462,578
;      FILING DATE: 09-JAN-1990
;SEQ ID NO:6:
;      LENGTH: 41
5177060-6

  Query Match             34.1%;  Score 61;  DB 6;  Length 41;
  Best Local Similarity   38.9%;  Pred. No. 0.013;
  Matches   14;  Conservative    7;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              :|:|:   ||| ::| || :  | ||  | : |  |
Db          6 ISIDLTFHLLRNMIEMARIENEREQAGLNRKYLDEV 41


RESULT 12
US-08-981-189B-8
; Sequence 8, Application US/08981189B
; Patent No. 6214797
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  UROCORTIN PEPTIDES
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FITCH, EVEN, TABIN & FLANNERY
;      STREET:  120 S. LaSalle Street, Suite 1600
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/981,189B
;      FILING DATE:  10-DEC-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/028,144
;      FILING DATE:  13-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/002,223
;      FILING DATE:  11-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Schumann, James J.
;      REGISTRATION NUMBER:  20,856
;      REFERENCE/DOCKET NUMBER:  57611
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  858-552-1311
;      TELEFAX:  858-552-0095
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-981-189B-8

  Query Match             33.5%;  Score 60;  DB 3;  Length 40;
  Best Local Similarity   44.4%;  Pred. No. 0.018;
  Matches   16;  Conservative    5;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          3 LSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
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Db          5 LSIDLTFHLLRTLLELARTQSQRERAEQNRIIFDSV 40
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RESULT 13
US-09-400-716-10
; Sequence 10, Application US/09400716
; Patent No. 6319900
; GENERAL INFORMATION:
; APPLICANT: Wei, Edward T.
; APPLICANT: Slominski, Andrzej T.
; TITLE OF INVENTION: INHIBITION OF ABNORMAL CELL GROWTH WITH
; TITLE OF INVENTION: CORTICOTROPIN-RELEASING HORMONE ANALOGS
; FILE REFERENCE: 2900.006US0
; CURRENT APPLICATION NUMBER: US/09/400,716
; CURRENT FILING DATE: 1999-09-21
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Rat
US-09-400-716-10

Query Match 33.5%; Score 60; DB 4; Length 40;
Best Local Similarity 44.4%; Pred. No. 0.018;
Matches 16; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 3 LSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
Db 5 LSIDLTFHLLRTLLELARTQSQRERAEQNRIIFDSV 40

RESULT 14
US-09-400-716-11
; Sequence 11, Application US/09400716
; Patent No. 6319900
; GENERAL INFORMATION:
; APPLICANT: Wei, Edward T.
; APPLICANT: Slominski, Andrzej T.
; TITLE OF INVENTION: INHIBITION OF ABNORMAL CELL GROWTH WITH
; TITLE OF INVENTION: CORTICOTROPIN-RELEASING HORMONE ANALOGS
; FILE REFERENCE: 2900.006US0
; CURRENT APPLICATION NUMBER: US/09/400,716
; CURRENT FILING DATE: 1999-09-21
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Human
US-09-400-716-11

Query Match 33.5%; Score 60; DB 4; Length 40;
Best Local Similarity 44.4%; Pred. No. 0.018;
Matches 16; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 3 LSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
Db 5 LSIDLTFHLLRTLLELARTQSQRERAEQNRIIFDSV 40

RESULT 15
US-09-356-139-3
; Sequence 3, Application US/09356139
; Patent No. 6680367
; GENERAL INFORMATION:
; APPLICANT: Desjardins, Clarissa
; TITLE OF INVENTION: FLUORESCENT CRF RECEPTOR-BINDING
; TITLE OF INVENTION: PEPTIDES
; FILE REFERENCE: 06942/022001
; CURRENT APPLICATION NUMBER: US/09/356,139
; CURRENT FILING DATE: 1999-07-19
; EARLIER APPLICATION NUMBER: 08/682,810
; EARLIER FILING DATE: 1996-07-10
; EARLIER APPLICATION NUMBER: 08/504,856
; EARLIER FILING DATE: 1995-07-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-356-139-3

Query Match 33.5%; Score 60; DB 4; Length 40;
Best Local Similarity 44.4%; Pred. No. 0.018;
Matches 16; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 3 LSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
Db 5 LSIDLTFHLLRTLLELARTQSQRERAEQNRIIFDSV 40

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Sequence: 1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	179	100.0	38	10	US-09-799-978-43	Sequence 43, Appl
3	179	100.0	38	14	US-10-099-766-9	Sequence 9, Appli
4	179	100.0	112	9	US-09-919-473-10	Sequence 10, Appl
5	140	78.2	38	14	US-10-315-964A-114	Sequence 114, App
6	140	78.2	38	14	US-10-317-251A-114	Sequence 114, App
7	140	78.2	38	14	US-10-317-252A-114	Sequence 114, App
8	139	77.7	38	9	US-09-919-473-4	Sequence 4, Appli
9	139	77.7	38	10	US-09-799-978-44	Sequence 44, Appl
10	139	77.7	38	14	US-10-099-766-8	Sequence 8, Appli
11	139	77.7	38	14	US-10-315-964A-4	Sequence 4, Appli
12	139	77.7	38	14	US-10-315-964A-123	Sequence 123, App
13	139	77.7	38	14	US-10-315-964A-354	Sequence 354, App
14	139	77.7	38	14	US-10-317-251A-4	Sequence 4, Appli
15	139	77.7	38	14	US-10-317-251A-123	Sequence 123, App
16	139	77.7	38	14	US-10-317-251A-354	Sequence 354, App
17	139	77.7	38	14	US-10-317-252A-4	Sequence 4, Appli
18	139	77.7	38	14	US-10-317-252A-123	Sequence 123, App
19	139	77.7	38	14	US-10-317-252A-354	Sequence 354, App
20	139	77.7	39	14	US-10-315-964A-356	Sequence 356, App
21	139	77.7	39	14	US-10-315-964A-368	Sequence 368, App
22	139	77.7	39	14	US-10-317-251A-356	Sequence 356, App
23	139	77.7	39	14	US-10-317-251A-368	Sequence 368, App
24	139	77.7	39	14	US-10-317-252A-356	Sequence 356, App
25	139	77.7	39	14	US-10-317-252A-368	Sequence 368, App
26	139	77.7	41	9	US-09-919-473-3	Sequence 3, Appli
27	139	77.7	112	9	US-09-682-706-2	Sequence 2, Appli
28	139	77.7	112	9	US-09-919-473-2	Sequence 2, Appli
29	138	77.1	38	14	US-10-315-964A-122	Sequence 122, App
30	138	77.1	38	14	US-10-317-251A-122	Sequence 122, App
31	138	77.1	38	14	US-10-317-252A-122	Sequence 122, App
32	137	76.5	38	14	US-10-315-964A-110	Sequence 110, App
33	137	76.5	38	14	US-10-317-251A-110	Sequence 110, App
34	137	76.5	38	14	US-10-317-252A-110	Sequence 110, App
35	136	76.0	38	14	US-10-315-964A-109	Sequence 109, App
36	136	76.0	38	14	US-10-315-964A-124	Sequence 124, App
37	136	76.0	38	14	US-10-315-964A-127	Sequence 127, App
38	136	76.0	38	14	US-10-315-964A-130	Sequence 130, App
39	136	76.0	38	14	US-10-317-251A-109	Sequence 109, App
40	136	76.0	38	14	US-10-317-251A-124	Sequence 124, App
41	136	76.0	38	14	US-10-317-251A-127	Sequence 127, App
42	136	76.0	38	14	US-10-317-251A-130	Sequence 130, App
43	136	76.0	38	14	US-10-317-252A-109	Sequence 109, App
44	136	76.0	38	14	US-10-317-252A-124	Sequence 124, App
45	136	76.0	38	14	US-10-317-252A-127	Sequence 127, App

ALIGNMENTS

RESULT 1
US-09-919-473-11
; Sequence 11, Application US/09919473
; Patent No. US20020127221A1
; GENERAL INFORMATION:
; APPLICANT: Vale, Wylie Walker Jr.
; APPLICANT: Lewis, Kathy Ann
; APPLICANT: Reyes, Teresa Marie
; APPLICANT: Hogenesch, John Beren
; APPLICANT: Sawchenko, Paul Emil
; APPLICANT: Vaughan, Joan Maureen
; APPLICANT: Rivier, Jean Edouard Frederic
; APPLICANT: Perrin, Marilyn Heller
; TITLE OF INVENTION: Urocortin Proteins and Uses Thereof
; FILE REFERENCE: D6334
; CURRENT APPLICATION NUMBER: US/09/919,473
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/273,969
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 11
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: Mouse Urocortin II
US-09-919-473-11

Query Match 100.0%; Score 179; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.6e-20;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
||||||||||||||||||||||||||||||||||||||
Db 1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38

RESULT 2

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US-09-799-978-43
; Sequence 43, Application US/09799978
; Publication No. US20030165807A1
; GENERAL INFORMATION:
;  APPLICANT:  The Procter & Gamble Company
;  APPLICANT:  Isfort, Robert
;  APPLICANT:  Sheldon, Russell
;  TITLE OF INVENTION:  Methods for Identifying Compounds for Regulating Muscle Mass or
;  TITLE OF INVENTION:  Function Using Corticotropin Releasing Factor Receptors
;  FILE REFERENCE:  8448
;  CURRENT APPLICATION NUMBER: US/09/799,978
;  CURRENT FILING DATE:  2001-03-06
;  NUMBER OF SEQ ID NOS:  44
;  SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 43
;  LENGTH: 38
;  TYPE: PRT
;  ORGANISM: Mus musculus
US-09-799-978-43

  Query Match            100.0%;  Score 179;  DB 10;  Length 38;
  Best Local Similarity  100.0%;  Pred. No. 2.6e-20;
  Matches   38;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              |||||||||||||||||||||||||||||||||||||
Db          1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38


RESULT 3
US-10-099-766-9
; Sequence 9, Application US/10099766
; Publication No. US20030036507A1
; GENERAL INFORMATION:
;  APPLICANT: Lewis, Kathy
;  APPLICANT:  Vale, Wylie
;  APPLICANT:  Marilyn H. Perrin
;  APPLICANT:  Jean E. Rivier
;  APPLICANT:  Koichi S. Kunitake
;  APPLICANT:  Joszef Gulyas
;  TITLE OF INVENTION: Urocortin III and Uses Thereof
;  FILE REFERENCE: D6390
;  CURRENT APPLICATION NUMBER: US/10/099,766
;  CURRENT FILING DATE:  2002-03-15
;  PRIOR APPLICATION NUMBER: US 60/276,069
;  PRIOR FILING DATE: 2001-03-15
;  NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 9
;  LENGTH: 38
;  TYPE: PRT
;  ORGANISM: Mus musculus
;  FEATURE:
;  OTHER INFORMATION: Mouse Urocortin II (mUcn II)
US-10-099-766-9

  Query Match            100.0%;  Score 179;  DB 14;  Length 38;
  Best Local Similarity  100.0%;  Pred. No. 2.6e-20;
  Matches   38;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              |||||||||||||||||||||||||||||||||||||
Db          1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38


RESULT 4
US-09-919-473-10
; Sequence 10, Application US/09919473
; Patent No. US20020127221A1
; GENERAL INFORMATION:
;  APPLICANT: Vale, Wylie Walker Jr.
;  APPLICANT:  Lewis, Kathy Ann
;  APPLICANT:  Reyes, Teresa Marie
;  APPLICANT:  Hogenesch, John Beren
;  APPLICANT:  Sawchenko, Paul Emil
;  APPLICANT:  Vaughan, Joan Maureen
;  APPLICANT:  Rivier, Jean Edouard Frederic
;  APPLICANT:  Perrin, Marilyn Heller
;  TITLE OF INVENTION: Urocortin Proteins and Uses Thereof
;  FILE REFERENCE: D6334
;  CURRENT APPLICATION NUMBER: US/09/919,473
;  CURRENT FILING DATE:  2001-07-31
;  PRIOR APPLICATION NUMBER: US 60/273,969
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 10
;  LENGTH: 112
;  TYPE: PRT
;  ORGANISM: Mus musculus
;  FEATURE:
;  OTHER INFORMATION: Mouse Urocortin II precursor peptide
US-09-919-473-10

  Query Match            100.0%;  Score 179;  DB 9;  Length 112;
  Best Local Similarity  100.0%;  Pred. No. 9.6e-20;
  Matches   38;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              |||||||||||||||||||||||||||||||||||||
Db         72 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 109


RESULT 5
US-10-315-964A-114
; Sequence 114, Application US/10315964A
; Publication No. US20030148956A1
; GENERAL INFORMATION:
;  APPLICANT: The Procter & Gamble Company
;  APPLICANT:  Isfort, Robert J
;  APPLICANT:  Mazur, Wieslaw A
;  TITLE OF INVENTION: Cortcotropin Releasing Factor 2 Receptor Agonists
;  FILE REFERENCE: 8847M3
;  CURRENT APPLICATION NUMBER: US/10/315,964A
;  CURRENT FILING DATE:  2003-04-01
;  PRIOR APPLICATION NUMBER: US 60/349,117
;  PRIOR FILING DATE: 2002-01-16
;  PRIOR APPLICATION NUMBER: US 60/376,337
;  PRIOR FILING DATE: 2002-04-29
;  PRIOR APPLICATION NUMBER: US 60/388,895
;  PRIOR FILING DATE: 2002-06-14
;  PRIOR APPLICATION NUMBER: US 60/411,988
;  PRIOR FILING DATE: 2002-09-19
;  NUMBER OF SEQ ID NOS: 530
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 114
;  LENGTH: 38
;  TYPE: PRT
;  ORGANISM: Artificial
;  FEATURE:
;  OTHER INFORMATION: Chemically synthesized artificial peptide
;  FEATURE:
;  NAME/KEY: MOD_RES
;  LOCATION: (38)..(38)
;  OTHER INFORMATION: AMIDATION
US-10-315-964A-114

  Query Match            78.2%;  Score 140;  DB 14;  Length 38;
  Best Local Similarity  76.3%;  Pred. No. 2.9e-14;
  Matches   29;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              ::|||||||||:|||||| :||| || |||:||| |
Db          1 IVLSLDVPIGLLQILLEQARQRAAREQATTNARILARV 38


RESULT 6
US-10-317-251A-114
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; Sequence 114, Application US/10317251A
; Publication No. US20030148957A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert J
; APPLICANT: Mazur, Wieslaw A
; TITLE OF INVENTION: Cortcotropin Releasing Factor 2 Receptor Agonists
; FILE REFERENCE: 8847M2
; CURRENT APPLICATION NUMBER: US/10/317,251A
; CURRENT FILING DATE: 2002-12-11
; PRIOR APPLICATION NUMBER: US 60/349,117
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: US 60/376,337
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/388,895
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/411,988
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 530
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 114
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized artificial peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (38)..(38)
; OTHER INFORMATION: AMIDATION
US-10-317-251A-114

Query Match 78.2%; Score 140; DB 14; Length 38;
Best Local Similarity 76.3%; Pred. No. 2.9e-14;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
::|||||||||||:|||||||:|||:||:|||:|||:|
Db 1 IVLSLDVPIGLLQILLEQARQRAAREQATTNARILARV 38

RESULT 7
US-10-317-252A-114
; Sequence 114, Application US/10317252A
; Publication No. US20030148958A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert J
; APPLICANT: Mazur, Wieslaw A
; TITLE OF INVENTION: Cortcotropin Releasing Factor 2 Receptor Agonists
; FILE REFERENCE: 8847M
; CURRENT APPLICATION NUMBER: US/10/317,252A
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/349,117
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: US 60/376,337
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/388,895
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/411,988
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 530
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 114
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized artificial peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (38)..(38)
; OTHER INFORMATION: AMIDATION
US-10-317-252A-114

Query Match 78.2%; Score 140; DB 14; Length 38;
Best Local Similarity 76.3%; Pred. No. 2.9e-14;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
::|||||||||||:|||||||:|||:||:|||:|||:|
Db 1 IVLSLDVPIGLLQILLEQARQRAAREQATTNARILARV 38

RESULT 8
US-09-919-473-4
; Sequence 4, Application US/09919473
; Patent No. US20020127221A1
; GENERAL INFORMATION:
; APPLICANT: Vale, Wylie Walker Jr.
; APPLICANT: Lewis, Kathy Ann
; APPLICANT: Reyes, Teresa Marie
; APPLICANT: Hogenesch, John Beren
; APPLICANT: Sawchenko, Paul Emil
; APPLICANT: Vaughan, Joan Maureen
; APPLICANT: Rivier, Jean Edouard Frederic
; APPLICANT: Perrin, Marilyn Heller
; TITLE OF INVENTION: Urocortin Proteins and Uses Thereof
; FILE REFERENCE: D6334
; CURRENT APPLICATION NUMBER: US/09/919,473
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/273,969
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 4
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amino acids 1-38 of human
; OTHER INFORMATION: Urocortin-related peptide (hURP)
US-09-919-473-4

Query Match 77.7%; Score 139; DB 9; Length 38;
Best Local Similarity 76.3%; Pred. No. 4.2e-14;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
::|||||||||||:|||||||:|||:||:|||:|||:|
Db 1 IVLSLDVPIGLLQILLEQARARAAREQATTNARILARV 38

RESULT 9
US-09-799-978-44
; Sequence 44, Application US/09799978
; Publication No. US20030165807A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert
; APPLICANT: Sheldon, Russell
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or
; TITLE OF INVENTION: Function Using Corticotropin Releasing Factor Receptors
; FILE REFERENCE: 8448
; CURRENT APPLICATION NUMBER: US/09/799,978
; CURRENT FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-978-44

Query Match 77.7%; Score 139; DB 10; Length 38;
Best Local Similarity 76.3%; Pred. No. 4.2e-14;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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Qy          1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              ::|||||||||||:|||||||  :|||  ||  |||:|||  |
Db          1 IVLSLDVPIGLLQILLEQARARAAREQATTNARILARV 38


RESULT 10
US-10-099-766-8
; Sequence 8, Application US/10099766
; Publication No. US20030036507A1
; GENERAL INFORMATION:
;  APPLICANT: Lewis, Kathy
;  APPLICANT:  Vale, Wylie
;  APPLICANT:  Marilyn H. Perrin
;  APPLICANT:  Jean E. Rivier
;  APPLICANT:  Koichi S. Kunitake
;  APPLICANT:  Joszef Gulyas
;  TITLE OF INVENTION: Urocortin III and Uses Thereof
;  FILE REFERENCE: D6390
;  CURRENT APPLICATION NUMBER: US/10/099,766
;  CURRENT FILING DATE:  2002-03-15
;  PRIOR APPLICATION NUMBER: US 60/276,069
;  PRIOR FILING DATE: 2001-03-15
;  NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 8
;   LENGTH: 38
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Human Urocortin-related peptide (hURP),
;   OTHER INFORMATION: human urocortin II
US-10-099-766-8

  Query Match             77.7%;  Score 139;  DB 14;  Length 38;
  Best Local Similarity   76.3%;  Pred. No. 4.2e-14;
  Matches   29;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              ::|||||||||||:|||||||  :|||  ||  |||:|||  |
Db          1 IVLSLDVPIGLLQILLEQARARAAREQATTNARILARV 38


RESULT 11
US-10-315-964A-4
; Sequence 4, Application US/10315964A
; Publication No. US20030148956A1
; GENERAL INFORMATION:
;  APPLICANT: The Procter & Gamble Company
;  APPLICANT:  Isfort, Robert J
;  APPLICANT:  Mazur, Wieslaw A
;  TITLE OF INVENTION: Cortcotropin Releasing Factor 2 Receptor Agonists
;  FILE REFERENCE: 8847M3
;  CURRENT APPLICATION NUMBER: US/10/315,964A
;  CURRENT FILING DATE:  2003-04-01
;  PRIOR APPLICATION NUMBER: US 60/349,117
;  PRIOR FILING DATE: 2002-01-16
;  PRIOR APPLICATION NUMBER: US 60/376,337
;  PRIOR FILING DATE: 2002-04-29
;  PRIOR APPLICATION NUMBER: US 60/388,895
;  PRIOR FILING DATE: 2002-06-14
;  PRIOR APPLICATION NUMBER: US 60/411,988
;  PRIOR FILING DATE: 2002-09-19
;  NUMBER OF SEQ ID NOS: 530
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 38
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-315-964A-4

  Query Match             77.7%;  Score 139;  DB 14;  Length 38;
  Best Local Similarity   76.3%;  Pred. No. 4.2e-14;
  Matches   29;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              ::|||||||||||:|||||||  :|||  ||  |||:|||  |
Db          1 IVLSLDVPIGLLQILLEQARARAAREQATTNARILARV 38


RESULT 12
US-10-315-964A-123
; Sequence 123, Application US/10315964A
; Publication No. US20030148956A1
; GENERAL INFORMATION:
;  APPLICANT: The Procter & Gamble Company
;  APPLICANT:  Isfort, Robert J
;  APPLICANT:  Mazur, Wieslaw A
;  TITLE OF INVENTION: Cortcotropin Releasing Factor 2 Receptor Agonists
;  FILE REFERENCE: 8847M3
;  CURRENT APPLICATION NUMBER: US/10/315,964A
;  CURRENT FILING DATE:  2003-04-01
;  PRIOR APPLICATION NUMBER: US 60/349,117
;  PRIOR FILING DATE: 2002-01-16
;  PRIOR APPLICATION NUMBER: US 60/376,337
;  PRIOR FILING DATE: 2002-04-29
;  PRIOR APPLICATION NUMBER: US 60/388,895
;  PRIOR FILING DATE: 2002-06-14
;  PRIOR APPLICATION NUMBER: US 60/411,988
;  PRIOR FILING DATE: 2002-09-19
;  NUMBER OF SEQ ID NOS: 530
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 123
;   LENGTH: 38
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Chemically synthesized artificial peptide
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (38)..(38)
;   OTHER INFORMATION: AMIDATION
US-10-315-964A-123

  Query Match             77.7%;  Score 139;  DB 14;  Length 38;
  Best Local Similarity   76.3%;  Pred. No. 4.2e-14;
  Matches   29;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              ::|||||||||||:|||||||  :|||  ||  |||:|||  |
Db          1 IVLSLDVPIGLLQILLEQARQEAAREQATTNARILARV 38


RESULT 13
US-10-315-964A-354
; Sequence 354, Application US/10315964A
; Publication No. US20030148956A1
; GENERAL INFORMATION:
;  APPLICANT: The Procter & Gamble Company
;  APPLICANT:  Isfort, Robert J
;  APPLICANT:  Mazur, Wieslaw A
;  TITLE OF INVENTION: Cortcotropin Releasing Factor 2 Receptor Agonists
;  FILE REFERENCE: 8847M3
;  CURRENT APPLICATION NUMBER: US/10/315,964A
;  CURRENT FILING DATE:  2003-04-01
;  PRIOR APPLICATION NUMBER: US 60/349,117
;  PRIOR FILING DATE: 2002-01-16
;  PRIOR APPLICATION NUMBER: US 60/376,337
;  PRIOR FILING DATE: 2002-04-29
;  PRIOR APPLICATION NUMBER: US 60/388,895
;  PRIOR FILING DATE: 2002-06-14
;  PRIOR APPLICATION NUMBER: US 60/411,988
;  PRIOR FILING DATE: 2002-09-19
;  NUMBER OF SEQ ID NOS: 530
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 354
;   LENGTH: 38
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;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Chemically synthesized artificial peptide
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: ACETYLATION
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (38)..(38)
;   OTHER INFORMATION: AMIDATION
US-10-315-964A-354

  Query Match             77.7%;  Score 139;  DB 14;  Length 38;
  Best Local Similarity   76.3%;  Pred. No. 4.2e-14;
  Matches   29;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              ::|||||||||||:|||||||  :||| ||  |||:||| |
Db          1 IVLSLDVPIGLLQILLEQARARAAREQATTNARILARV 38


RESULT 14
US-10-317-251A-4
; Sequence 4, Application US/10317251A
; Publication No. US20030148957A1
; GENERAL INFORMATION:
;  APPLICANT: The Procter & Gamble Company
;  APPLICANT:  Isfort, Robert J
;  APPLICANT:  Mazur, Wieslaw A
;  TITLE OF INVENTION: Cortcotropin Releasing Factor 2 Receptor Agonists
;  FILE REFERENCE: 8847M2
;  CURRENT APPLICATION NUMBER: US/10/317,251A
;  CURRENT FILING DATE:  2002-12-11
;  PRIOR APPLICATION NUMBER: US 60/349,117
;  PRIOR FILING DATE: 2002-01-16
;  PRIOR APPLICATION NUMBER: US 60/376,337
;  PRIOR FILING DATE: 2002-04-29
;  PRIOR APPLICATION NUMBER: US 60/388,895
;  PRIOR FILING DATE: 2002-06-14
;  PRIOR APPLICATION NUMBER: US 60/411,988
;  PRIOR FILING DATE: 2002-09-19
;  NUMBER OF SEQ ID NOS: 530
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 38
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-317-251A-4

  Query Match             77.7%;  Score 139;  DB 14;  Length 38;
  Best Local Similarity   76.3%;  Pred. No. 4.2e-14;
  Matches   29;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              ::|||||||||||:|||||||  :||| ||  |||:||| |
Db          1 IVLSLDVPIGLLQILLEQARARAAREQATTNARILARV 38


RESULT 15
US-10-317-251A-123
; Sequence 123, Application US/10317251A
; Publication No. US20030148957A1
; GENERAL INFORMATION:
;  APPLICANT: The Procter & Gamble Company
;  APPLICANT:  Isfort, Robert J
;  APPLICANT:  Mazur, Wieslaw A
;  TITLE OF INVENTION: Cortcotropin Releasing Factor 2 Receptor Agonists
;  FILE REFERENCE: 8847M2
;  CURRENT APPLICATION NUMBER: US/10/317,251A
;  CURRENT FILING DATE:  2002-12-11
;  PRIOR APPLICATION NUMBER: US 60/349,117
;  PRIOR FILING DATE: 2002-01-16
;  PRIOR APPLICATION NUMBER: US 60/376,337
;  PRIOR FILING DATE: 2002-04-29
;  PRIOR APPLICATION NUMBER: US 60/388,895
;  PRIOR FILING DATE: 2002-06-14
;  PRIOR APPLICATION NUMBER: US 60/411,988
;  PRIOR FILING DATE: 2002-09-19
;  NUMBER OF SEQ ID NOS: 530
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 123
;   LENGTH: 38
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Chemically synthesized artificial peptide
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (38)..(38)
;   OTHER INFORMATION: AMIDATION
US-10-317-251A-123

  Query Match             77.7%;  Score 139;  DB 14;  Length 38;
  Best Local Similarity   76.3%;  Pred. No. 4.2e-14;
  Matches   29;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 VILSLDVPIGLLRILLEQARYKAARNQAATNAQILAHV 38
              ::|||||||||||:|||||||  :||| ||  |||:||| |
Db          1 IVLSLDVPIGLLQILLEQARQEAAREQATTNARILARV 38


Search completed: April 20, 2004, 19:06:54
Job time : 20.5067 secs
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